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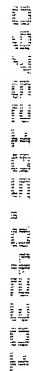


Figure 1A

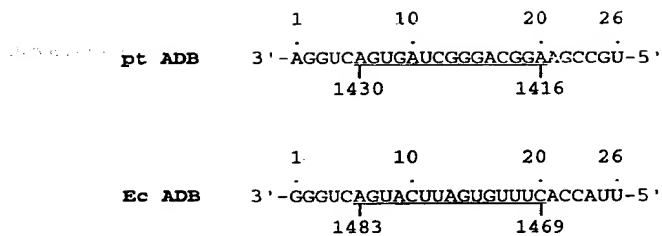


Figure 1B

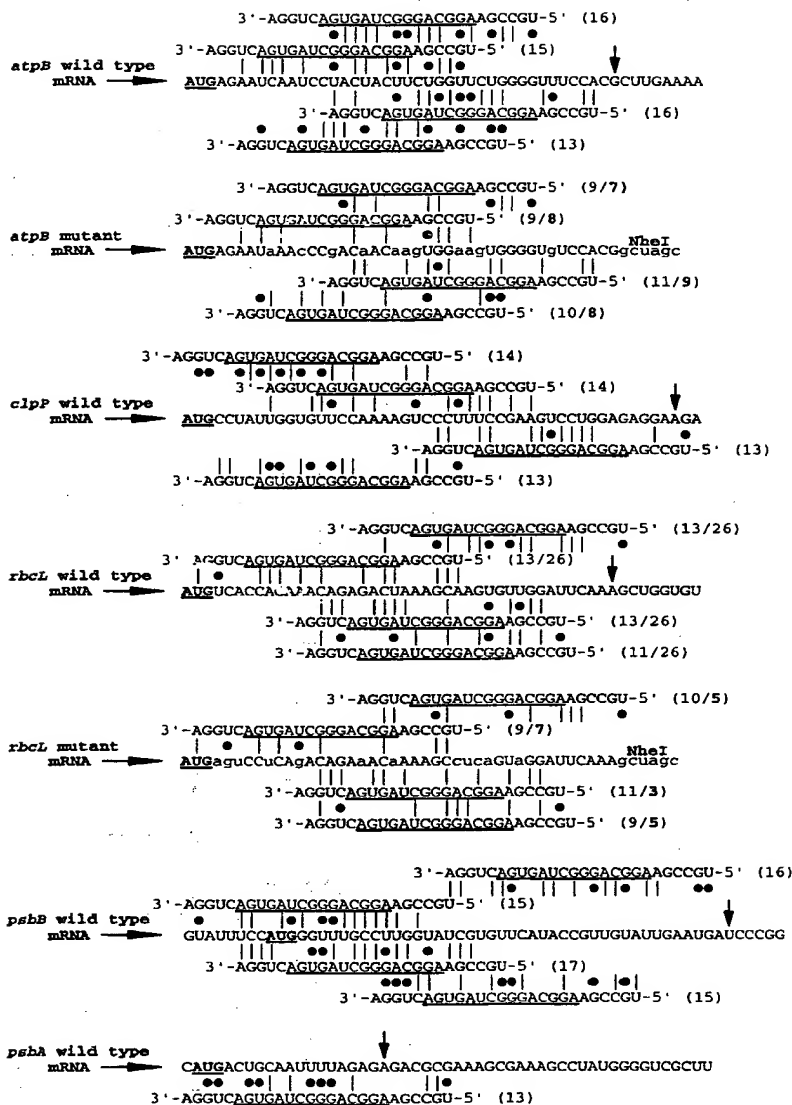


Figure 2A



Figure 2B

PrnLclpP-DB (pHK13)

1 SacI
gagctcGCTC CCCC GCCC GTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TTACGTTTCC NheI
101 ACCTCAAAGT GAAATATAGT ATTTAGTTCT TTCTTTCATT TAATGCCTgc
151 tagc

Figure 3A

PrrnLrbcl+DBwt (pHK14)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
101 CTTGTGTGTTG TGAAaATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
NheI
151 TCACCACAAA CAGAGACTAA AGCAAGTGT GGATTCAAAG ctagc

PrrnLrbcl-DB (pHK15)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
101 CTTGTGTGTTG TGAAaATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
NheI
151 TCAGctagc

PrrnLrbcl+DBm (pHK54)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
101 CTTGTTGTGTTG TGAAaATTCT TAATTCATGA GTTGTAGGGA GGGATTTATG
NheI
151 aguCCuCAgA CAGAAaCaAA AGCcucaGTa GGATTCAAAG ctagc

PrrnLpsbB+DBwt (pHK16)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAATGCAATA
101 AAGTTACGTA GTGTCTATTT ATCTTTGATA TAAGGGGTAT TTCCATGGGT
NheI
151 TTGCCTTGGT ATCGTGTTCa TACCGTTGTA TTGAATGATg ctagc

PrrnLpsbB-DB (pHK17)

SacI
1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAATGCAATA
NcoI NheI
101 AAGTTACGTA GTGTCTATTT ATCTTTGATA TAAGGGGTAT TTccatggct
151 agc

Figure 3B

PrrnLpsbA+DBwt (pHK21)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAA AAAAGCCTTC
 101 CATTTTCTAT TTTGATTTGT AGAAAACTAG TGTGCTTGGG AGTCCCTGAT
 151 GATTAAATAA ACCAAGATTT TACCATGACT GCAATTTTAG AGAGAgctag
 201 c

PrrnLpsbA-DB (pHK22)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAA AAAAGCCTTC
 101 CATTTTCTAT TTTGATTTGT AGAAAACTAG TGTGCTTGGG AGTCCCTGAT
 151 GATTAAATAA ACCAAGATTT TAccatggct agc

PrrnLpsbA-DB(+GC) (pHK23)

SacI
 1 gagctcGCTC CCCC GCCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG CAAAAAGCCT
 101 TCCATTTTCT ATTTTGATTT GTAGAAACT AGTGTGCTTG GGAGTCCCTG
 151 ATGATTAAAT AAACCAAGAT TTTAccatgg ctacg

Figure 3C

09/762105
 PCT/US99/17806
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1 gagctcCTC CCCCGGCGTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
51 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
101 ACGGTTTCCC aCTAGAAATA ATTTTGTTTA ACTTTAAGAA GGAGATATAC
151 ATATGgctag c

Figure 3D

9/49

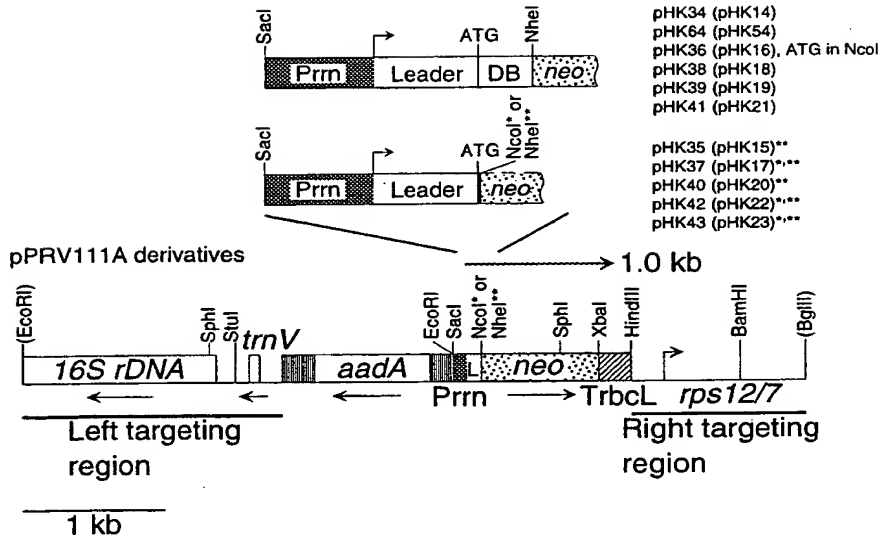


Figure 4A

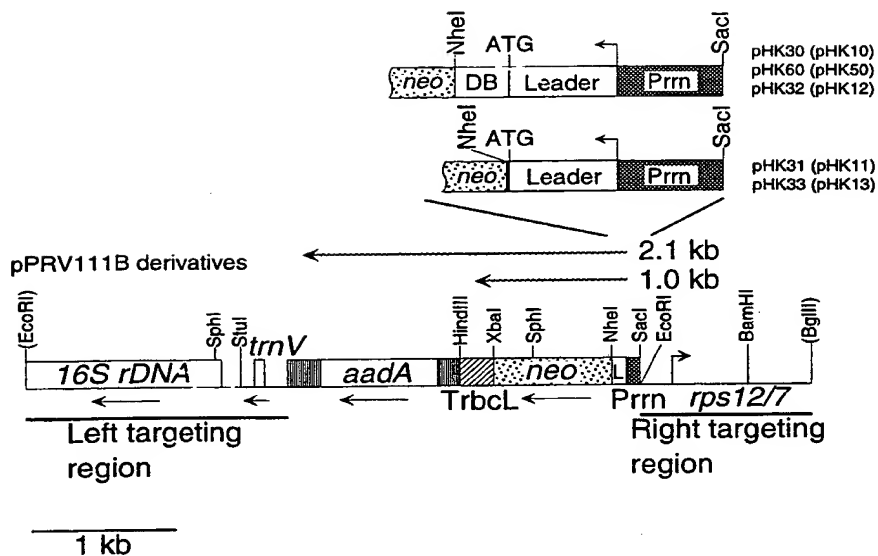
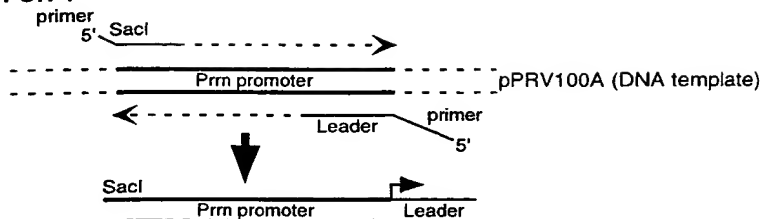
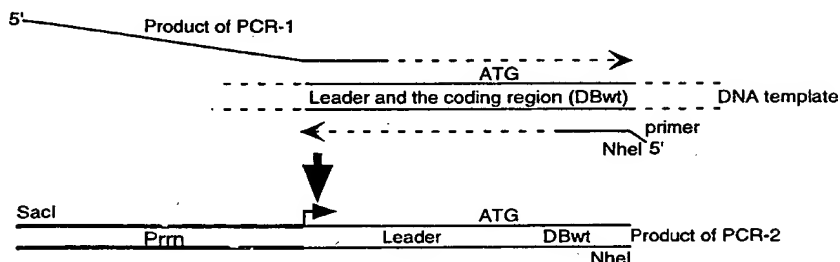
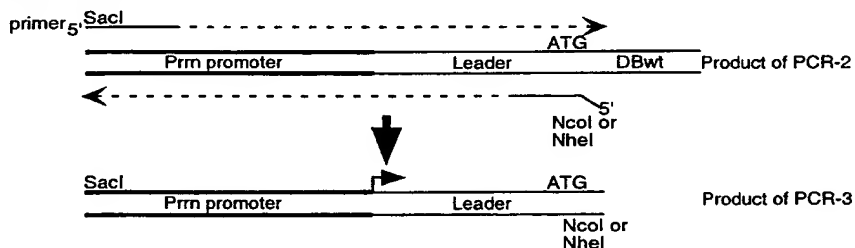
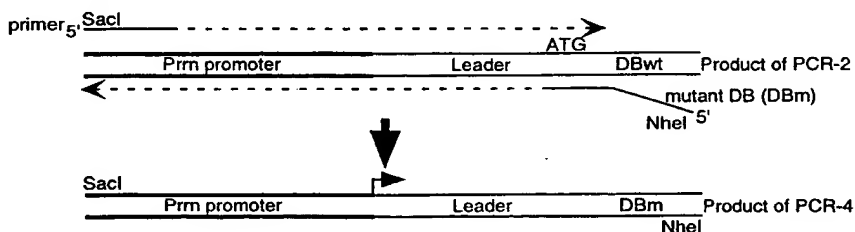


Figure 4B

PCR-1**PCR-2: Construct with wild-type DB (DBwt)****PCR-3: Construct without DB****PCR-4: Construct with mutant DB (DBm)****Figure 5**

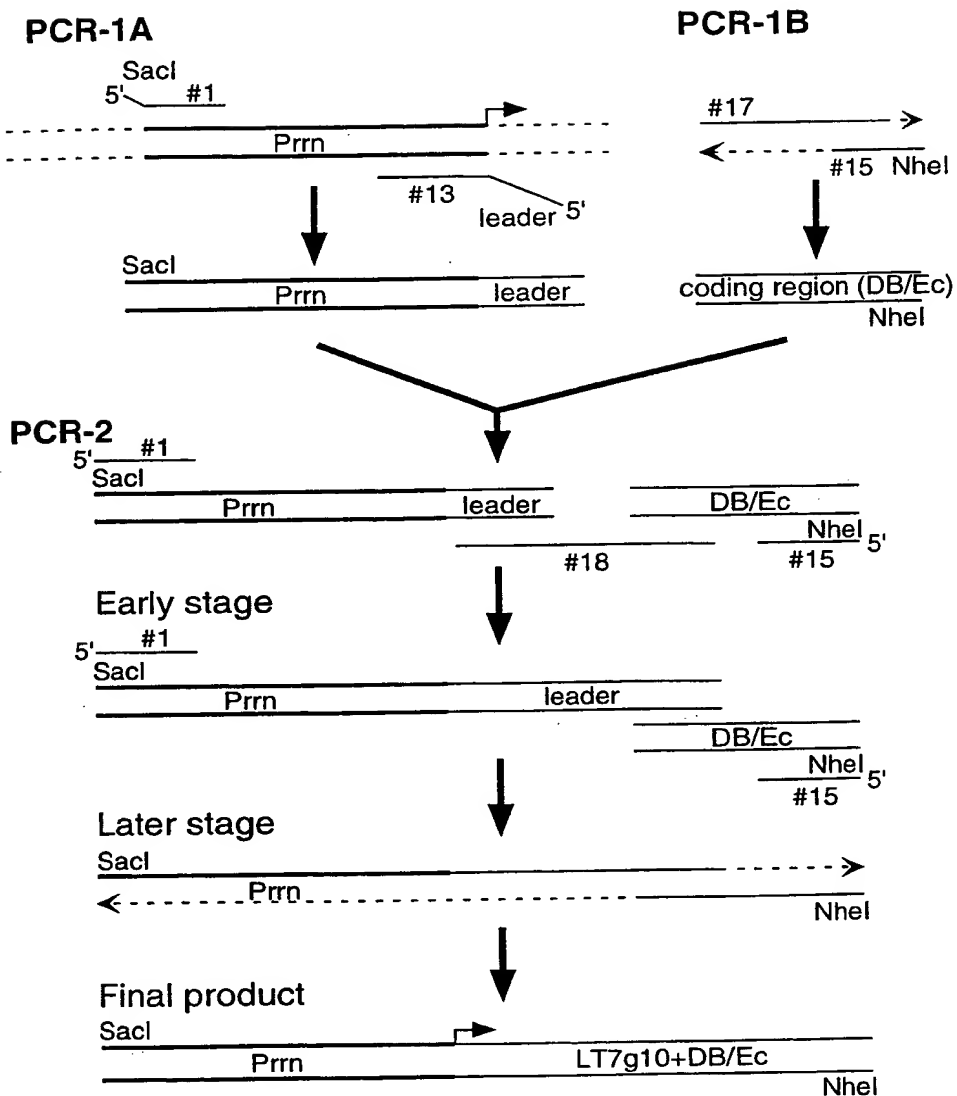


Figure 6

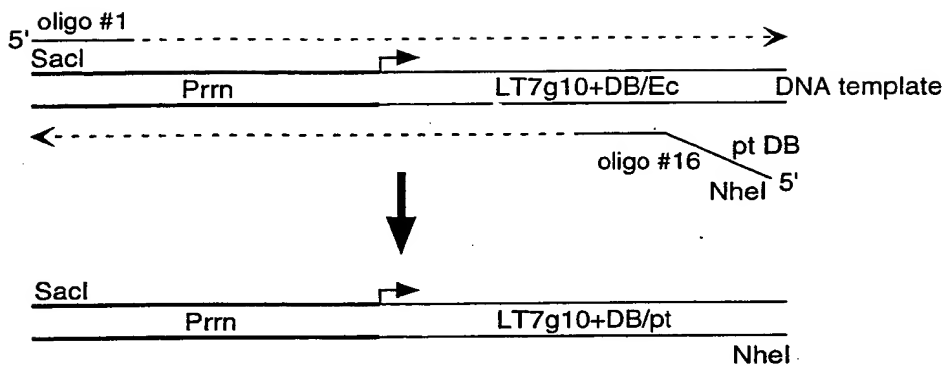


Figure 7

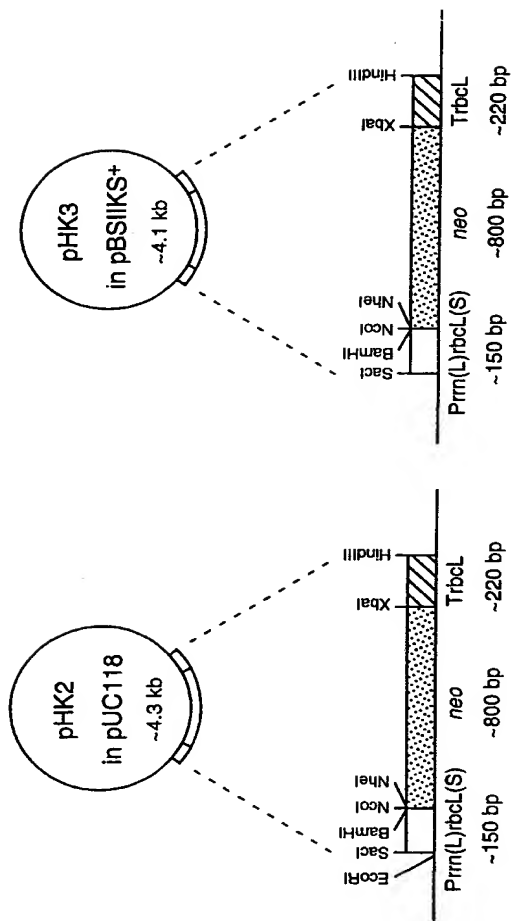


Figure 8

1 **SacI**
 gagctcggta cccaaaGCTC CCCCGCCGTC GTTCAATGAG AATGGATAAG
 51 AGGCTCGTGG GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG
 101 CGAACTCCGG GCGAATAcGA AGCGCtTGGA TACAGTTGTA GGGAGGGATc **NcoI**
 NheI
 151 catggctagc ATTGAACAAG ATGGATTGCA CGCAGGTTCT CCGGCCGCTT
 201 GGGTGGAGAG GCTATTCCGC TATGACTGGG CACAACAGAC AATCGGCTGC
 251 TCTGATGCCG CCGTGTTCGG GCTGTCAGCG CAGGGGCGCC CGGTTCTTTT
 301 TGTCAAGACC GACCTGTCCG GTGCCCTGAA TGAActCCAG GACGAGGCAG
 351 CGCGGCTATC GTGGCTGGCC ACGACGGGCG TTCCTTGCGC AGCTGTGCTC
 401 GACGTTGTCA CTGAAGCGGG AAGGGACTGG CTGCTATTGG GCGAAGTGCC
 451 GGGGCAGGAT CTCCTGTCAT CTCACCTTGC TCCTGCCGAG AAAGTATCCA
 501 TCATGGCTGA TGCAATGCGG CGGCTGCATA CGCTTGATCC GGCTACCTGC
 551 CCATTCGACC ACCAAGCGAA ACATCGCATC GAGCGAGCAC GTACTCGGAT
 601 GGAAGCCGGT CTTGTGCGATC AGGATGATCT GGACGAAGAG CATCAGGGGC
 651 TCGCGCCAGC CGAACTGTTC GCCAGGCTCA AGGCGCGCAT GCCCCACGGC
 701 GAGGATCTCG TCGTGACACA TGGCGATGCC TGCTTGCCGA ATATCATGGT
 751 GGAAAAATGGC CGCTTTTCTG GATTCATCGA CTGTGGCCGG CTGGGTGTGG
 801 CGGACCGCTA TCAGGACATA GCGTTGGCTA CCCGTGATAT TGCTGAAGAG
 851 CTTGGCGGCG AATGGGCTGA CCGCTTCCTC GTGCTTTACG GTATCGCCGC
 901 TCCCGATTTCG CAGCGCATCG CCTTCTATCG CCTTCTTGAC GAGTTCTTCT
 XbaI
 951 GAgcgggtct agagtAGACA TTAGCAGATA AATTAGCAGG AAATAAAGAA
 1001 GGATAAGGAG AAAGAACTCA AGTAATTATC CTTTCGTTCTC TTAATTGAAT
 1051 TGCAATTAAA CTCGGCCCAA TCTTTTACTA AAAGGATTGA GCCGAATACA
 1101 ACAAAGATTC TATTGCATAT ATTTTGACTA AGTATATACT TACCTAGATA
 HindIII
 1151 TACAAGATTT GAAATACAAA ATCTAGcaag ctt

Figure 9

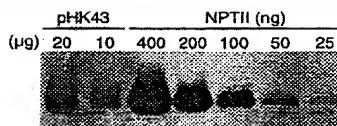
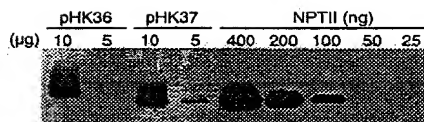
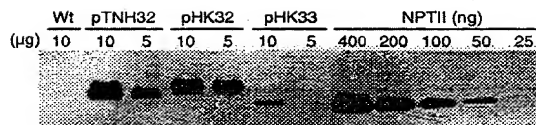
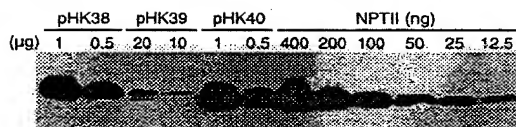
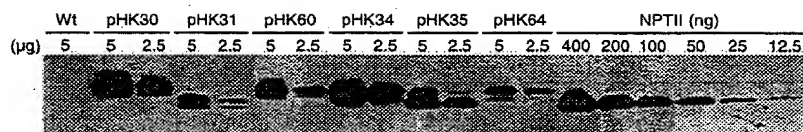


Figure 10

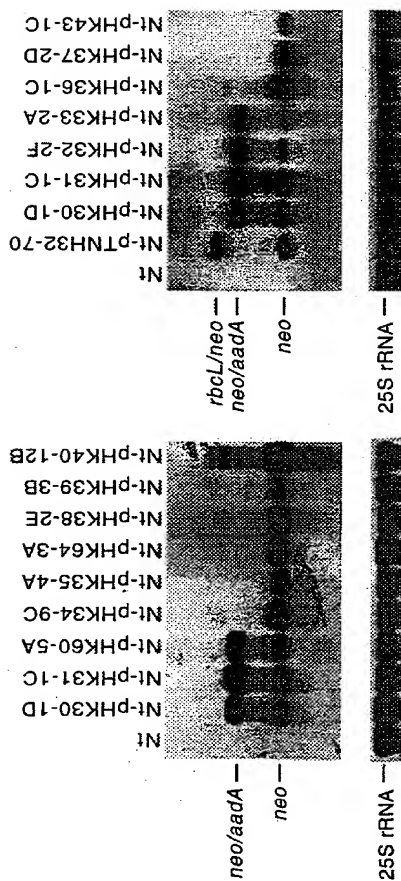


Figure 11

PCT/US99/17806

atpB wt	AUG	AGA	AUC	AAU	CCU	ACU	ACU	UCU	GGU	UCU	GGG	GUU	UCC	ACG
	Met	Arg	Ile	Asn	Pro	Thr	Thr	Ser	Gly	Ser	Gly	Val	Ser	Thr
	1.0	0.22	0.27	0.61	0.30	0.37	0.37	0.31	0.38	0.31	0.26	0.35	0.14	0.15
Fraction														
Triplet/1000	24.6	7.8	15.5	18.1	13.5	18.4	18.4	20.2	28.2	20.2	19.2	24.9	9.1	7.5
atpB m	AUG	AGA	AUA	AAC	CCG	ACA	ACA	agu	Gga	agu	GGG	GUG	UCC	ACG
	Met	Arg	Ile	Asn	Pro	Thr	Thr	Ser	Gly	Ser	Gly	Val	Ser	Thr
	1.0	0.22	0.29	0.39	0.30	0.23	0.23	0.14	0.24	0.14	0.26	0.21	0.14	0.15
Fraction														
Triplet/1000	24.6	7.8	16.6	11.4	13.2	11.7	11.7	9.3	17.9	9.3	19.2	15.3	9.1	7.5
rbcL wt	AUG	UCA	CCA	CAA	ACA	GAG	ACU	AAA	GCA	AGU	GUU	GGA	UUC	AAA
	Met	Ser	Pro	Gln	Thr	Glu	Thr	Lys	Ala	Ser	Val	Gly	Phe	Lys
	1.0	0.21	0.24	0.57	0.23	0.38	0.37	0.60	0.29	0.14	0.35	0.24	0.40	0.60
Fraction														
Triplet/1000	24.6	13.5	10.6	21.0	11.7	12.4	18.4	22.0	18.1	9.3	24.9	17.9	22.5	22.0
rbcL m	AUG	agu	CCU	CAG	ACA	GAA	ACA	AAA	GCC	uca	GUA	GGA	UUC	AAA
	Met	Ser	Pro	Gln	Thr	Glu	Thr	Lys	Ala	Ser	Val	Gly	Phe	Lys
	1.0	0.14	0.30	0.43	0.23	0.62	0.23	0.60	0.16	0.21	0.31	0.24	0.40	0.60
Fraction														
Triplet/1000	24.6	9.3	13.5	15.5	11.7	20.7	11.7	22.0	10.1	13.5	21.8	17.9	22.5	22.0
T7g10+DB/EC	AUG	GCa	AGC	AUG	ACU	GGU	GGA	CAG	gcu	agc	auu	gaa	caa	gau
	Met	Ala	Ser	Met	Thr	Gly	Gly	Gln	Ala	Ser	Ile	Glu	Gln	Asp
	1.0	0.29	0.07	1.00	0.37	0.38	0.24	0.43	0.39	0.07	0.45	0.62	0.57	0.75
Fraction														
Triplet/1000	24.6	18.1	4.7	24.6	18.4	28.2	17.9	15.5	24.4	4.7	25.9	20.7	21.0	24.6
T7g10+DB/pt	AUG	GCa	Auc	acu	agc	ccu	gcc	uug	gcu	agc	auu	gaa	caa	gau
	Met	Ala	Ile	Thr	Ser	Pro	Ala	Leu	Ala	Ser	Ile	Glu	Gln	Asp
	1.0	0.29	0.27	0.37	0.07	0.30	0.16	0.24	0.39	0.07	0.45	0.62	0.57	0.75
Fraction														
Triplet/1000	24.6	18.1	15.5	18.4	4.7	13.5	10.1	34.7	24.4	4.7	25.9	20.7	21.0	24.6
T7g10-DB	AUG	gcu	agc	auu	gaa	caa	gau	gga	uug	cac	gca	ggg	ucu	ccg
	Met	Ala	Ser	Ile	Glu	Gln	Asp	Gly	Leu	His	Ala	Gly	Ser	Pro
	1.0	0.39	0.07	0.45	0.62	0.57	0.75	0.24	0.24	0.28	0.29	0.38	0.31	0.30
Fraction														
Triplet/1000	24.6	24.4	4.7	25.9	20.7	21.0	24.6	17.9	34.7	9.1	18.1	28.2	20.2	13.2

Figure 12

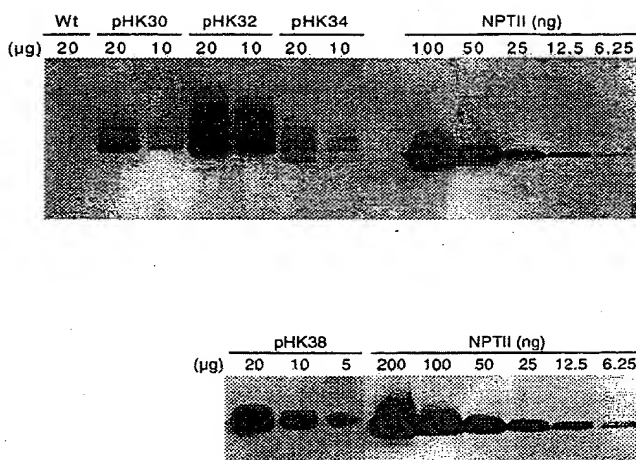


Figure 13A

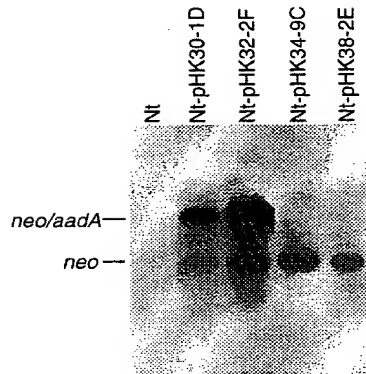


Figure 13B

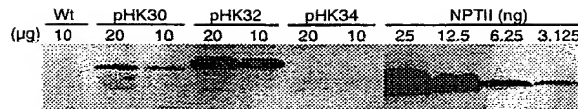


Figure 14

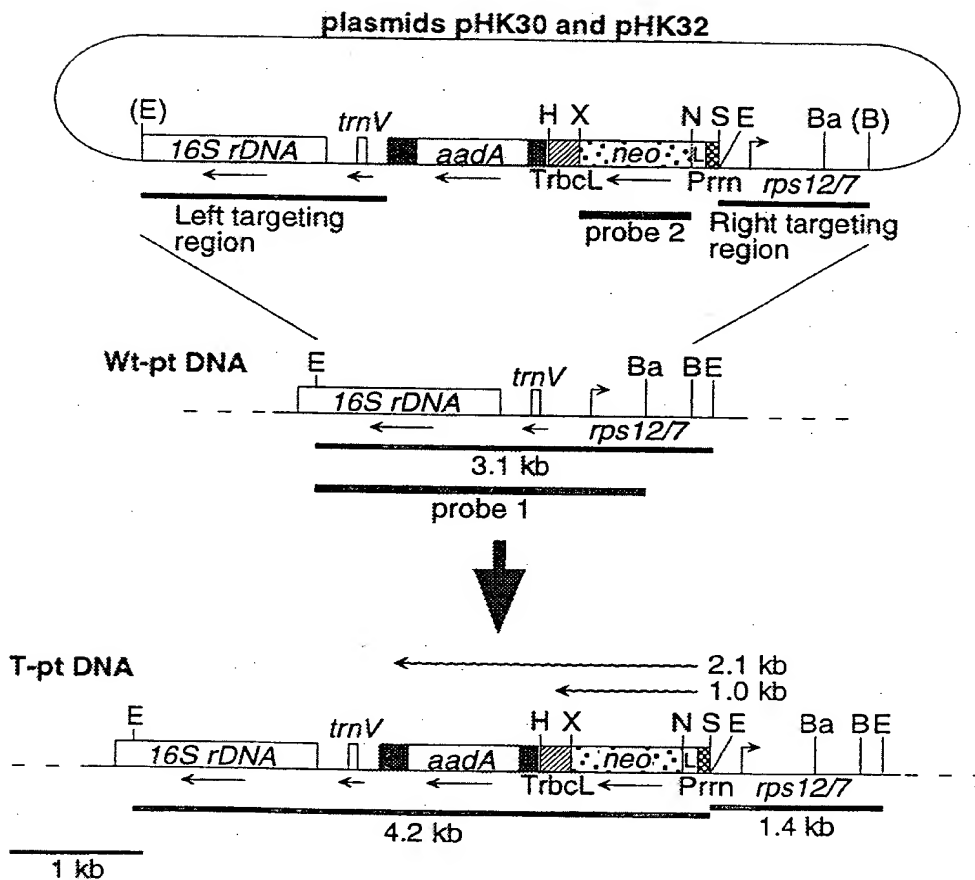


Figure 15A

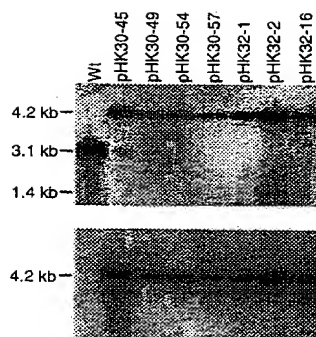


Figure 15B

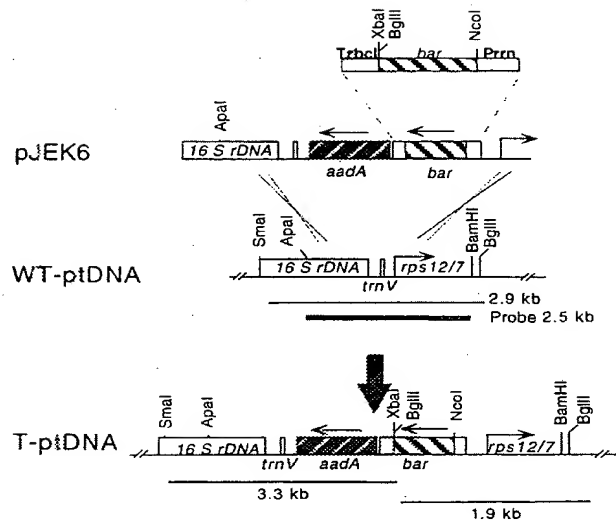


Figure 16A

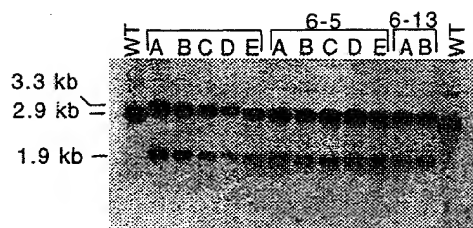


Figure 16B

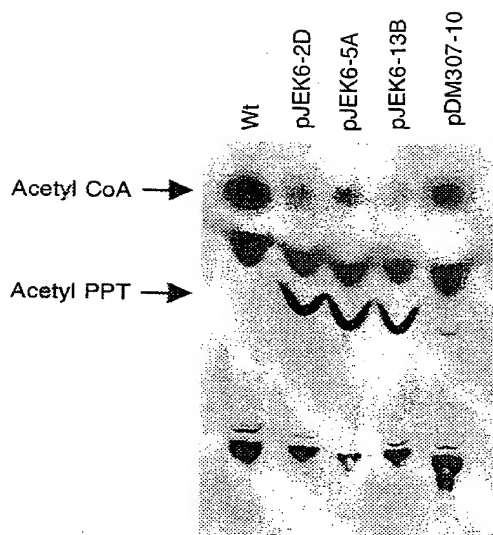


Figure 17

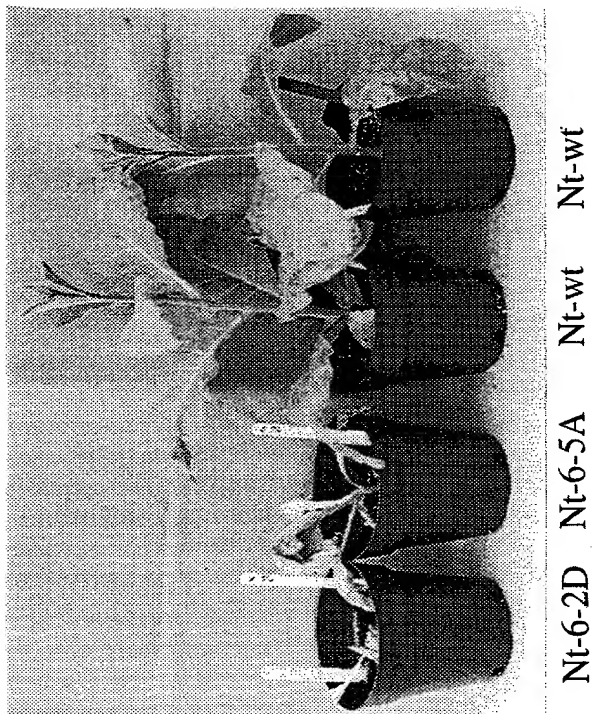


Figure 18A

FIG. 18B

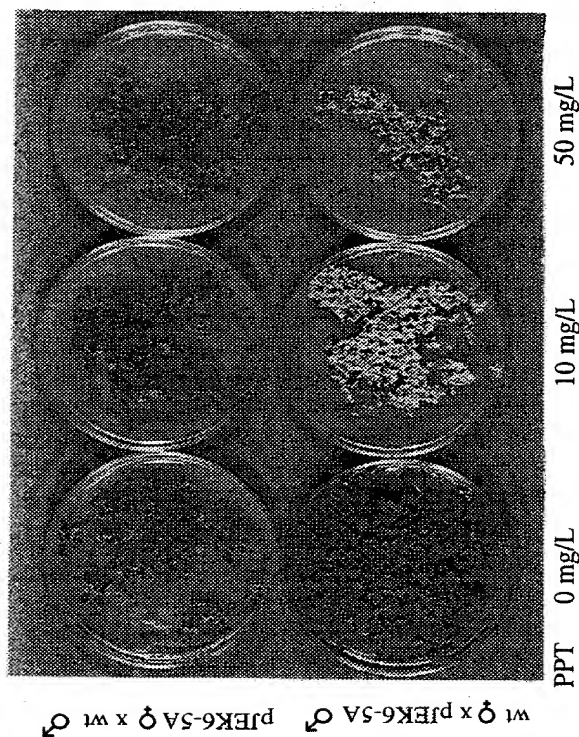


Figure 18B

NcoI

CCATGgcaccacaaacagagAGCCCAGAACGACGCCCCGCCGACATCCGCCGTGCCACCG
 -----+-----+-----+-----+-----+-----+ 60
 GGTACggtggtgttgtctcTCGGGTCTTGCTGCGGGCCGGCTGTAGGCGGCACGGTGGC
 M A P Q T E S P E R R P A D I R R A T E
 AGGCGGACATGCCGGCGGTCTGCACCATCGTCAACCACTACATCGAGACAAGCACGGTCA
 -----+-----+-----+-----+-----+-----+ 120
 TCCGCCTGTACGGCCGCCAGACGTGGTAGCAGTTGGTGATGTAGCTCTGTTCTGTGCCAGT
 A D M P A V C T I V N H Y I E T S T V N
 ACTTCCGTACCGAGCCGAGGAACCGCAGGAGTGACGGACGACCTCGTCCGTCTGCGGG
 -----+-----+-----+-----+-----+-----+ 180
 TGAAGGCATGGCTCGGCGTCTTGGCGTCCTCACCTGCCTGCTGGAGCAGGCAGACGCCC
 F R T E P Q E P Q E W T D D L V R L R E
 AGCGCTATCCCTGGCTCGTCGCCGAGGTGGACGGCGAGGTGCGCCGCATCGCCTACGCGG
 -----+-----+-----+-----+-----+-----+ 240
 TCGCGATAGGGACCGAGCAGCGGCTCCACCTGCCGCTCCAGCGCCGTAGCGGATGCGCC
 R Y P W L V A E V D G E V A G I A Y A G
 GCCCCTGGAAGGCACGCAACGCCTACGACTGGACGGCCGAGTCGACCGTGTACGTCTCCC
 -----+-----+-----+-----+-----+-----+ 300
 CGGGGACCTTCCGTGCGTGTGCGGATGCTGACCTGCCGGCTCAGCTGGCACATGCAGAGGG
 P W K A R N A Y D W T A E S T V Y V S P
 CCCGCCACCGAGCGGACGGGACTGGGCTCCACGCTCTACACCCACCTGCTGAAGTCCCTGG
 -----+-----+-----+-----+-----+-----+ 360
 GGGCGGTGGTTCGCCTGCCCTGACCCGAGGTGCGAGATGTGGGTGGACGACTTCAGGGACC
 R H Q R T G L G S T L Y T H L L K S L E
 AGGCACAGGGCTTCAAGAGCGTGGTTCGCTGTCATCGGGCTGCCAACGACCCGAGCGTGC
 -----+-----+-----+-----+-----+-----+ 420
 TCCGTGTCCCGAAGTTCTCGCACCAGCGACAGTAGCCCGACGGGTGCTGGGCTCGCACG
 A Q G F K S V V A V I G L P N D P S V R
 GCATGCACGAGGCGCTCGGATATGCCCCCGCGGCATGCTGCGGGCGGCCGGCTTCAAGC
 -----+-----+-----+-----+-----+-----+ 480
 CGTACGTGCTCCGCGAGCCTATACGGGGGGCGCCGTACGACGCCCCGCGGCCGAAGTTCTG
 M H E A L G Y A P R G M L R A A G F K H
 ACGGGAAGTGGCATGACGTGGGTTTCTGGCAGCTGGACTTCAGCCTGCCGGTACCGCCCC
 -----+-----+-----+-----+-----+-----+ 540
 TGCCTTGACCGTACTGCACCCAAAGACCGTCGACCTGAAGTCGGACGGCCATGGCGGGG
 G N W H D V G F W Q L D F S L P V P P R

BglII

GTCCGGTCTGCCCGTCACCGAGATCTGATGAtcgaattcctgcagcccggggatccac
 -----+-----+-----+-----+-----+-----+ 600
 CAGGCCAGGACGGGCGAGTGGCTCTAGACTACTagcttaaggacgtcgggccccctaggtg
 P V L P V T E I *

XbaI

tagttctaga
 -----+ 610
 atcaagatct

Figure 19

Bg1III
XbaI
 CcGTtACTGAGATCTGATGatctaga
 -----+-----+-----
 GgCAaTGaCTCTAGACTACTagatct
 V T E I * *

Figure 20A

Parameter	Unit	Value	Unit	Value	Unit	Value	Unit	Value
α	deg	10.0	β	deg	10.0	γ	deg	10.0
δ	deg	10.0	ϵ	deg	10.0	ζ	deg	10.0
η	deg	10.0	θ	deg	10.0	ι	deg	10.0
κ	deg	10.0	λ	deg	10.0	μ	deg	10.0
ν	deg	10.0	ξ	deg	10.0	\omicron	deg	10.0
π	deg	10.0	ρ	deg	10.0	σ	deg	10.0
τ	deg	10.0	υ	deg	10.0	ϕ	deg	10.0
χ	deg	10.0	ψ	deg	10.0	ω	deg	10.0
Ω	deg	10.0	Λ	deg	10.0	Σ	deg	10.0
Φ	deg	10.0	Υ	deg	10.0	Ψ	deg	10.0
Ξ	deg	10.0	Θ	deg	10.0	Ω	deg	10.0
Γ	deg	10.0	Δ	deg	10.0	Σ	deg	10.0
Π	deg	10.0	Υ	deg	10.0	Φ	deg	10.0
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Λ	deg	10.0	Ξ	deg	10.0	Θ	deg	10.0
Σ	deg	10.0	Γ	deg	10.0	Δ	deg	10.0
Ψ	deg	10.0	Φ	deg	10.0	Ω	deg	10.0
Φ	deg	10.0	Ω	deg	10.0	Λ	deg	10.0
Ω	deg	10.0	Λ	deg	10.0	Σ	deg	10.0
Λ	deg	10.0	Σ	deg	10.0	Ψ	deg	10.0
Σ	deg	10.0	Ψ	deg	10.0	Φ	deg	10.0
Ψ	deg	10.0	Φ	deg	10.0	Ω	deg	10.0
Φ	deg	10.0	Ω	deg	10.0	Λ	deg	10.0
Ω	deg	10.0	Λ	deg	10.0	Σ	deg	10.0
Λ	deg	10.0	Σ	deg	10.0	Ψ	deg	10.0
Σ	deg	10.0	Ψ	deg	10.0	Φ	deg	10.0
Ψ	deg	10.0	Φ	deg	10.0	Ω	deg	10.0
Φ	deg	10.0	Ω	deg	10.0	Λ	deg	10.0
Ω	deg	10.0	Λ	deg	10.0	Σ	deg	10.0
Λ	deg	10.0	Σ	deg	10.0	Ψ	deg	10.0
Σ	deg	10.0	Ψ	deg	10.0	Φ	deg	10.0
Ψ	deg	10.0	Φ	deg	10.0	Ω	deg	10.0
Φ	deg	10.0	Ω	deg	10.0	Λ	deg	10.0
Ω	deg	10.0	Λ	deg	10.0	Σ	deg	10.0
Λ	deg	10.0	Σ	deg	10.0	Ψ	deg	10.0

NcoI NheI

ccATGgctAGCCAGAAAGAAgACCGGCCGATATtAGaCGTGCTACaGAAGctGATATGC
 +-----+
 ggTACcgaTCGGGTCTTtCTtCtGGCGGCTaTaatCtGCACGaTgtCtTCGaCTaTACG
 M A S P E R R P A D I R R A T E A D M P

CaGCaGTtTGtACaAAtGTtAATCATtATaTAgAAACAAgTACaGTaAATTTtCGaACTG
 +-----+
 GtCGTCAaACaTGTtAaCAaTTaGTaATaTATCTtTGTTCaTGtCATtTAAagCtTtGaC
 A V C T I V N H Y I E T S T V N F R T E

AaCctCAaGAACctCAaGAaTGGACtGAtGAttTaGTaCGTtTaCGaGAaCGtTATCCTt
 +-----+
 TtGGaGTtCTTGGaGTtCTtACCTGaCTaCTaaAtCATGCAaATGctCTtGCaATAGGaA
 P Q E P Q E W T D D L V R L R E R Y P W

GGCTtGTaGCaGAaGTtGACGGaGAaGTaGCTGGaATtGCaTATGctGGtCCgTGGAAaG
 +-----+
 CCGAaCATCGtCTtCAaCTGcCTtCTtCATCGaCCTTaaCGtATaCGaCCaGGcACCTTtC
 L V A E V D G E V A G I A Y A G P W K A

CACGaAATGCaTATGATtGGACaGCTGAaTCaACTGTtTATGTtTCaCCaCGtCATCAaC
 +-----+
 GTgCtTTaCGtATaCTaACCTGTtCGaCTtAGtTGaCAaATaCAaAGtGGtGCaGTaGTtG
 R N A Y D W T A E S T V Y V S P R H Q R

GtACaGGACTtGGtTCTtCACTtTaTATaCTtCATCTtCTtAAAAtCtTGGAAaGCACaAGGtT
 +-----+
 CaTGTtCCTGAaCCaAGaTGaaATaTATGaCTaGAaGAaTTtAGaaACCTtCGTGTtCCaA
 T G L G S T L Y T H L L K S L E A Q G F

TtAAaAGtGTaGTaGCTGTtTaTAgGatTGCCgAATGATCCctcaGTaCGCATGCATGAaG
 +-----+
 AaTTtTCaCATtCATCGACaATATCCtaACGGcTTaCTaGGgagtCATGCGTACGTaCTtC
 K S V V A V I G L P N D P S V R M H E A

CtCtTGATATGCTCCcaGaGGtATGtTGaGGGCaGCaGGtTTCAaACaTGGAaATtGGCC
 +-----+
 GaGAaCCTATACGaGGgtCtCCaTACaACTCCCGtCGtCCaAGTtGTaCCtTTaACCG
 L G Y A P R G M L R A A G F K H G N W H

ATGATGTaGGTTTTtTGGCAaCTtGAcTTCTtTtTaCCaGTACCTCCTCGTCCcGTtTtTAc
 +-----+
 TACTaCATCCAAaAACCGTtGAaCTgAACgagaaAtGGtCATGGaGGaGCAGGgCAaaatG
 D V G F W Q L D F S L P V P P R P V L P

BglIII XbaI

CcGTtACTGAGATCTGATGATctaga

GgCAaTGaCTCTAGACTACTagatct
 V T E I * *

Figure 20B

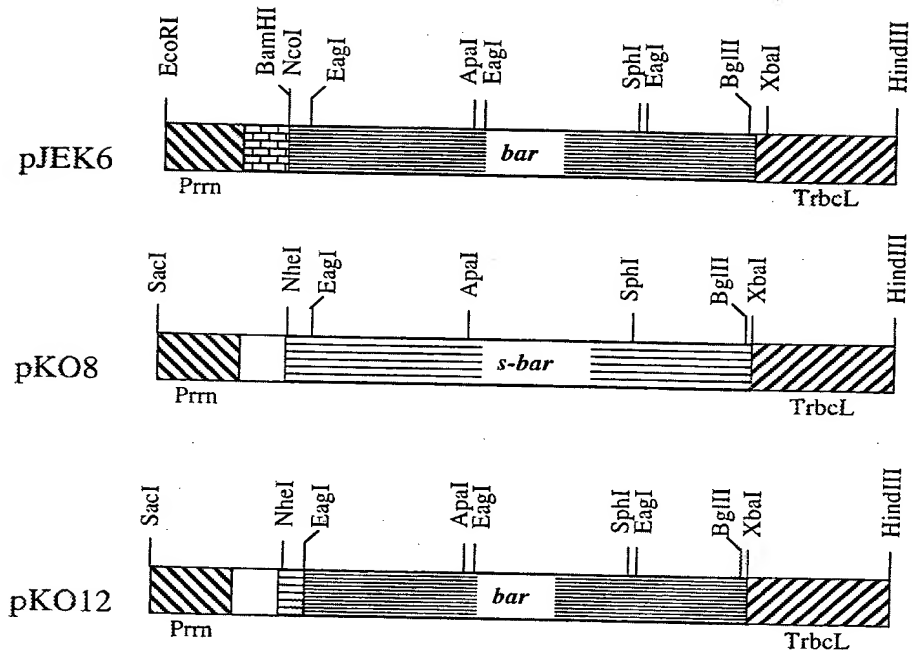


Figure 21

Bacterial Extracts

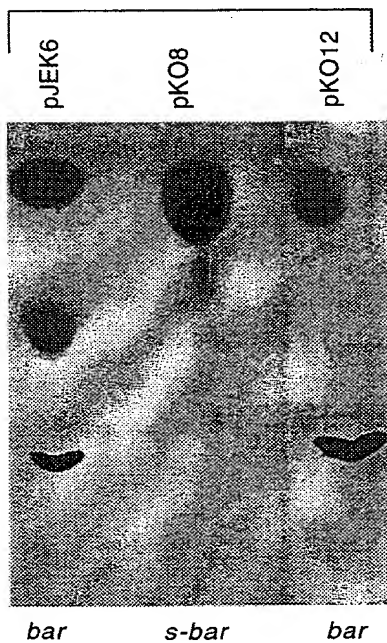


Figure 22A

Plant Extracts



Figure 22B

AAD E L V E G K L E L V E G L K V A GFP
 GGTAGTGGCAAAgaactgttgaggaaattggagctagtagaagggtcttaaagtcgCCATGG
 BstXI NcoI

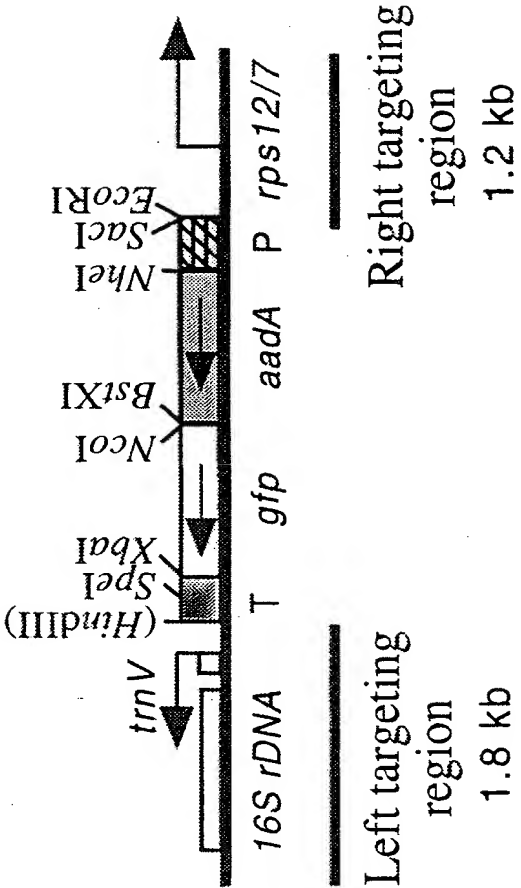


Figure 23A

Figure 23B

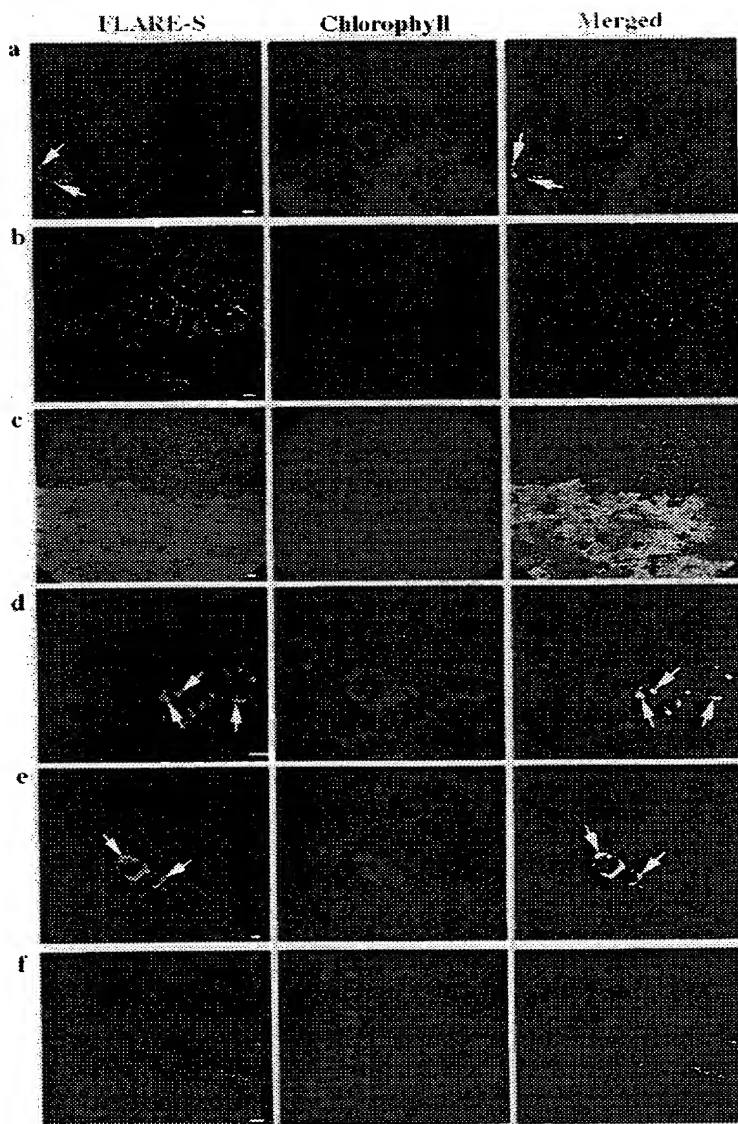


Figure 24

MW (kD)	GFP (ng)				AAD-GFP (mg)						
	400	200	100	50	25	12.5	Ni-pMSK56	Ni-pMSK57	Ni		
							10	5	2.5	1.25	10

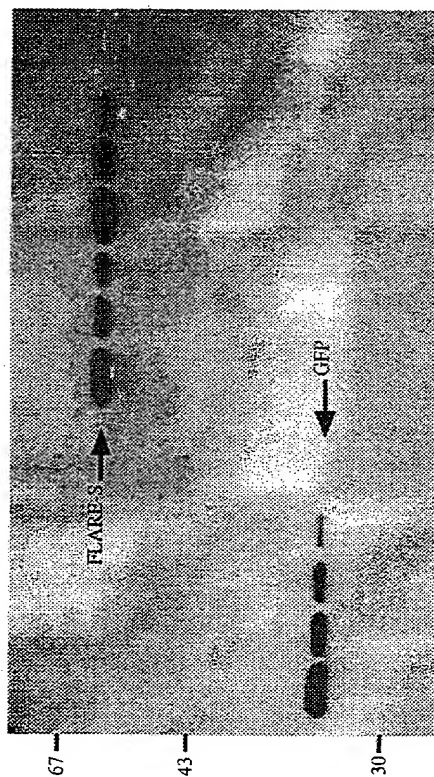


Figure 25

38/49

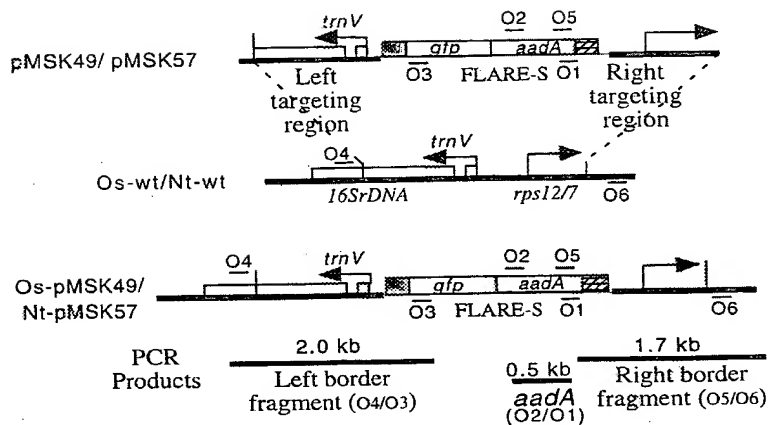


Figure 26A

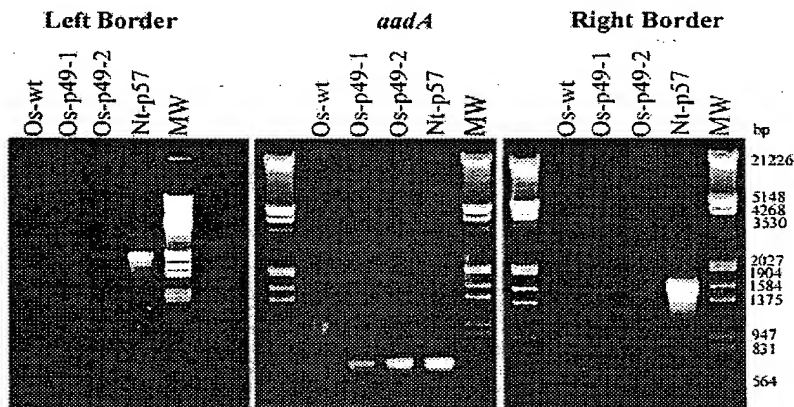


Figure 26B

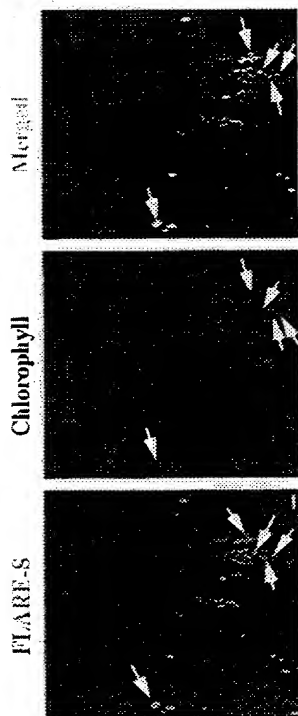


Figure 27

09762105 0929260

FLARE16-S.seq Length: 1574

1 ccATGgGGgc tagcGAAGCG GTGATCGCCG AAGTATCGAC TCAACTATCA
 51 GAGGTAGTTG GCGTCATCGA GCGCCATCTC GAACCGACGT TGCTGGCCGT
 101 ACATTTGTAC GGCCTCCGAG TGGATGGCGG CCTGAAGCCA CACAGTGATA
 151 TTGATTTGCT GGTACGGTG ACCGTAAAGC TTGATGAAC AACCGCGCGA
 201 GCCTTGATCA ACGACCTTTT GGAAACTTCG GCCTCCCTG GAGAGAGCGA
 251 GATTCTCCGC GCTGTAGAAG TCACCATTGT TGTGCACGAC GACATCATTC
 301 CGTGGCGTTA TCCAGCTAAG CGCGAACTGC AATTGGGAGA ATGGCAGCGC
 351 AATGACATTG TTGAGGTAT CTTGAGCCA GCCACGATCG ACATTGATCT
 401 GGCTATCTTG CTGACAAAAG CAAGAGAACA TAGCGTTGCC TTGGTAGGTC
 451 CAGCGCGCGA GGAACCTTTT GATCCGGTTC CTGAACAGGA TCTATTTGAG
 501 GCGCTAAATG AAACCTTAAC GCTATGGAAC TCGCCGCCCG ACTGGGCTGG
 551 CGATGAGCGA AATGTAGTGC TTACGTTGTC CCGCATTGG TACAGCGCAG
 601 TAACCGGCAA AATCGCGCCG AAGGATGTCG CTGCCGACTG GGCAATGGAG
 651 CGCTGCCCG CCCAGTATCA GCCCGTCATA CTTGAAGCTA GACAGGCTTA
 701 TCTTGACAA GAAGAAGATC GCTTGGCCTC GCGCGCAGAT CAGTTGGAAG
 751 AATTGTCCA CTACGTGAAA GCGGAGATCA CCAAGGTAGT ggGCAAAgaa
 801 cttgttgaag gaaaattgga gctagtagaa ggtcttaaag tgcgcctggc
 851 TAGTAAAGCA GAAGAATTT TCACTGGAGT TGTCCCAAT CTGTGTGAAT
 901 TAGATGGTGA TGTTAATGGG CACAAATTTT CTGTCACTGG AGAGGGTGAA
 951 GGTGATGCAA CATACGGAAA ACTTACCCTT AAATTTATTT GCACTACTGG
 1001 AAAACTACCT GTTCCTTGGC CAACACTTGT CACTACTTTC TCTTATGGTG
 1051 TTCAATGCTT TTCAAGATAC CCAGATCATA TGAAGCGGCA CGACTTCTTC
 1101 AAGAGCGCCA TGCTGAGGG ATACGTGCAG GAGAGGACCA TCTCTTTCAA
 1151 GGACGACGGG AACTACAGA CACGTGCTGA AGTCAAGTTT GAGGGAGACA
 1201 CCTCGTCAA CAGGATCGAG CTTAAGGGAA TCGATTTCAA GGAGGACGGA
 1251 AACATCCTCG GCCACAAGTT GGAATACAC TACAACCTCC ACAACGTATA
 1301 CATCACGGCA GACAAACAAA AGAATGGAAT CAAAGCTAAC TTCAAAATTA
 1351 GACACAACAT TGAAGATGGA AGCGTTCAAC TAGCAGACCA TTATCAACAA
 1401 AATACTCCAA TTGGCGATGG CCTGTCTT TTACCAGACA ACCATTACCT
 1451 GTCCACACAA TCTGCCCTTT CGAAAGATCC CAACGAAAAG AGAGACCACA
 1501 TGTCCTTCT TGAGTTTGA ACAGCTGCTG GGATTACACA TGGCATGGAT
 1551 GAACTATACA AATAAGcttc taga

XbaI

Figure 28

FLARE16-S1.seq Length: 1953

1 **SacI**
 51 gaggctcgcctc ccccgccgctc gtccaatgag aatggataag aggctcgtgg
 101 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG TCGAGTAGAC
 151 CTTGTTGTTG TGaaAATTCT TAATTCATGA GTTGTAGGGA GGGATTATG
 201 TCACCACAAA CAGAGACTAA AGCAAGTGT GgATTCAAA ctaggcgaagc
 251 GGTGATCGCC GAAGTATCGA CTCAACTATC AGAGGTAGTT GCGCTCATCG
 301 AGCGCCATCT CGAACCAGC TTGCTGGCCG TACATTTGTA CCGCTCCGCA
 351 GTGGATGGCG GCCTGAAGCC ACACAGTGAT ATTGATTTGC TGTTACCGT
 401 GACCGTAAGG CTTGATGAAA CAACGCGCGG AGCTTTGATC AACGACCTTT
 451 TGGAAACTTC GGCTTCCCCT GGAGAGAGCG AGATTCTCCG CGCTGTAGAA
 501 GTCACCATTC TTGTGCACGA CGACATCATT CCGTGGCGTT ATCCAGCTAA
 551 GCGCGAACTG CAATTGGAG AATGGCAGCG CAATGACATT CTTCAGGTA
 601 TCTTCGAGCC AGCCACGATC GACATTGATC TGGCTATCTT GCTGACAAA
 651 GCAAGAGAAC ATAGCGTTGC CTTGGTAGGT CCAGCGGCGG AGGAACTCTT
 701 TGATCCGGTT CCTGAACAGG ATCTATTTGA GCGCGTAAAT GAAACCTTAA
 751 CGCTATGGAA CTCGCCGCC GACTGGGCTG GCGATGAGCG AAATGTAGTG
 801 CTTACGTTGT CCCGATTTC GTACAGCGCA GTAACCGGCA AAATCGCGCC
 851 GAAGGATGTC GCTGCCGACT GGGCAATGGA GCGCCTGCCG GCCCAGTATC
 901 AGCCCGTCAT ACTTGAAGCT AGACAGGCTT ATCTTGGACA AGAAGAGAT
 951 CGCTTGGCCT CGCGCGCAGA TCAGTTGGAA GAATTGTCC ACTACGTGAA
 1001 AGGCGAGATC ACCAAGGTAG TcGGCAAA ga acttggtgaa ggaacttgg
 1051 agctagtaga aggtcttaaa gtccgctggtg ctAGTAAAGG AGAAGAACTT
 1101 TTCACTGGAG TTGTCCCAAT TCTTGTGAA TTAGATGGTG ATGTTAATGG
 1151 GCACAAATTT TCTGTCACTG GAGAGGGTGA AGGTGATGCA ACATACGGAA
 1201 AACTTACCCT TAAATTTATT TGCACACTG GAAAACCTACC TGTTCCCTGG
 1251 CCAACACTTG TCACTACTTT CTCTTATGGT GTTCAATGCT TTTCAAGATA
 1301 CCCAGATCAT ATGAAGCGGC ACGACTTCTT CAAGAGCGCC ATGCCTGAGG
 1351 GATACGTGCA GGAGAGGACC ATCTCTTTCA AGGACGACGG GAACTACAAG
 1401 ACACGTGCTG AAGTCAAGTT TGAGGGAGAC ACCCTCGTCA ACAGGATCGA
 1451 GCTTAAGGGA ATCGATTCA AGGAGGACGG AAACATCCTC GGCCACAAGT
 1501 TGGAATACAA CTACAACCTC CACAACGTAT ACATCACGGC AGACAAACAA
 1551 AAGAATGGAA TCAAAGCTAA CTTCAAAATT AGACACAACA TTGAAGATGG
 1601 AAGCGTCAA CTAGCAGACC ATTATCAACA AAATACTCCA ATTGGCGATG
 1651 GCCCTGTCTT TTACCAGAC AACCATTACC TGTCCACACA ATCTGCCCTT
 1701 TCGAAAGATC CCAACGAAA GAGAGACCAC ATGGTCTTTC TTGAGTTGT
 1751 AACAGCTGCT GGGATTACAC ATGGCATGGA TGAACATAC AAATAAGgct
 1801 ctagagcctat CTTGCCCTAG TCTATAGGAG GTTTTGAAA GAAAGGAGCA
 1851 ATAATCATTT TCTTGTCTTA TCAAGAGGGT GCTATTGCTC CTTTCTTTT
 1901 TTCTTTTAT TTAATTACTA GTATTTTACT TACATAGACT TTTTGTTTA
 1951 CATTATAGAA AAAGAAGGAG AGGTTATTTT CTTCATTAT TTCATGaaag
 ctt

Lsp808

ada

JfP

TpsbA

Hind III

Figure 29

FLARE16-S2.seq Length: 1985

SacI

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101	tcgacgtgca	agcggacatt	tattttaaat	tcgataattt	ttgcaaaaac
151	atttcgacat	atttatttat	tttattatta	tgagaatcaa	tcctactact
201	ttctggttcg	gggtttccac	ggctagcga	gcggtgatcg	ccgaagtatc
251	gactcaacta	tcagaggtag	ttggcgctat	cgagcgccat	ctcgaaccga
301	cgttgctggc	cgtagacttg	tacggctccg	cagtggatgg	cgccctgaag
351	ccacacagtg	atattgattt	gctggttacg	gtgaccgtaa	ggcttgatga
401	aacacgctgg	cgagctttga	tcacgacact	tttgaaact	tcggcttccc
451	ctggagagag	cgagattctc	cgcgctgtag	aagtcaccat	tgttgtgcac
501	gacgacatca	ttccgtggcg	ttatccagct	aagcgcgaac	tgcaatttgg
551	agaatggcag	cgcaatgaca	ttcttgacag	tatcttcgag	ccagccacga
601	tcgcacattga	tctggctatc	ttgctgacaa	aagcaagaga	acatagcgtt
651	gccttggtag	gtccagcggc	ggaggaactc	tttgatccgg	ttcctgaaca
701	ggatctattt	gaggcgctaa	atgaaacctt	aacgctatgg	aactcgccgc
751	ccgactgggc	tgccgatgag	cgaaatgtag	tgcttacgtt	gtccccatt
801	tggtacagcg	cagtaaccgg	caaaatcgcg	ccgaaggatg	tcgctgccga
851	ctgggcaatg	gagcgccctgc	cgcccacgta	tcagcccgtc	atacttgaag
901	ctagacaggc	ttatctngga	caagaagaag	atcgcttggc	ctcgccgcga
951	gatcagttgg	aagaatttgt	ccactacgtg	aaaggcgaga	tcaccaaggt
1001	agtcggcga	gaacttggtg	aaggaaaatt	ggaactagta	gaaggtctta
1051	aagtcgcct	ggctagtata	ggagaagaac	tttctactgg	agttgtccca
1101	attcttggtg	aattagatgg	tgatgttaat	gggcacaaat	tttctgtcag
1151	tggagagggg	gaaggtgatg	caacatacgg	aaaacttacc	cttaaattta
1201	tttgacttac	tggaaaacta	cctgttccct	ggccaaact	tgctactact
1251	ttctcttatg	gtgttcaatg	cttttcaaga	taccacagatc	atatgaagcg
1301	gcacgacttc	ttcaagagcg	ccatgcctga	gggatacgtg	caggagagga
1351	ccatctcttt	caaggacgac	gggaactaca	agacacgtgc	tgaagtcaag
1401	tttgaggagg	acaccctcgt	cracagatc	gagcttaagg	gaatcgattt
1451	caaggaggac	ggaaacatcc	tcggccacaa	gttggatatac	aactacaact
1501	cccacacgt	atacatcagc	gcagacaaac	aaaagaatgg	aatcaaaagt
1551	aaacttcaaaa	ttagacacaa	cattgaagat	ggaagcggtc	aactagcaga
1601	ccattatcaa	caaaatactc	caattggcga	tggccctgtc	ctttttaccg
1651	acaaccatta	cctgtccaca	caatctgccc	tttcgaaaga	tcccacgaa
1701	argagagacc	acatggctct	tcttgagttt	gtaacagctg	ctgggattac
1751	acatggcatg	gatgaactat	acaaataagg	ctctagagcg	atcctggcct
1801	agctctatagg	aggttttgaa	agaaaaggag	caataatcat	tttctgtgtc
1851	tatcaagagg	gtgctattgc	tcctttcctt	ttttcttttt	attttattac
1901	tagtatTTTA	cttacaTAgA	ctttttTgTt	tacattTatag	aaaagaagGg
1951	agaggttatt	ttcttgcatT	tattcatgaa	agctt	

L762105

aadA

gfp

T762105

HindIII

Figure 30

FLARE11-S.seq Length: 1595

NcoI C-Myc
 1 ccattgggggc tagcgaacaa aaactcattt ctgaagaaga cttagcctagc
 51 GAAGCGGTGA TCGCCGAAGT ATCGACTCAA CTATCAGAGG TAGTTGGCGT
 101 CATCGAGCGC CATCTCGAAC CGACGTTGCT GGCCGTACAT TTGTACGGCT
 151 CCGCAGTGGT TGGCGGCGCTG AAGCCACACA GTGATATTGA TTTGCTGGTT
 201 ACGGTGACCG TAAGGCTTGA TGAACAACCG CGGCGAGCTT TGATCAACGA
 251 CCTTTTGGA ACTTCGGCTT CCCCTGGAGA GAGCGAGATT CTCCGCGCTG
 301 TAGAAGTCAC CATTGTTGTG CACGACGACA TCATTCCGTG GCGTTATCCA
 351 GCTAAGCGCG AACTGCAATT TGGAGAATGG CAGCGCAATG ACATTCTTGC
 401 AGGTATCTTC GAGCCAGCCA CGATCGACAT TGATCTGGCT ATCTTGCTGA
 451 CAAAAGCAAG AGAACATAGC GTTGCCTTGG TAGGTCACG GGCGGAGGAA
 501 CTCTTTGATC CGGTTCTTGA ACAGGATCTA TTTGAGGCGC TAAATGAAAC
 551 CTTAACGCTA TGGAACTCGC CGCCCGACTG GGCTGGCGAT GAGCGAAATG
 601 TAGTGCTTAC GTTGTCCCGC ATTTGGTACA GCGCAGTAAC CGGCAAATC
 651 GCGCCGAAGG ATGTGCGCTG CCACTGGGCA ATGGAGCGCC TGCCGGCCCA
 701 GTATCAGCCC GTCATACTTG AAGCTAGACA GGCTTATCTT GGACAAGAAG
 751 AAGATCGCTT GGCCTCGCGC GCAGATCAGT TGGAGAATT TGTCCACTAG
 801 GTGAAGGCG AGATCACCAG GGTAGTGGC AAAGaaacttg cagtgaagg
 851 aaaattggag ctgcgcATGg cTAGTAAAGG AGAAGAACTT TTCACTGGAG
 901 TTGTCGAAT TCTTGTGAA TTAGATGGTG ATGTTAATGG GCACAAATTT
 951 TCTGTCAAGT JAGAGGGTGA AGGTGATGCA ACATACGGAA AACTTACCCT
 1001 TAAATTTATT TGCACTACTG GAAACTACC TGTTCCTTGG CCAACACTTG
 1051 TCACACTATT CTCTTATGGT GTTCAATGCT TTTCAAGATA CCCAGATCAT
 1101 ATGAAGCGGC ACGACTTCTT CAAGAGCGCC ATGCCTGAGG GATACGTGCA
 1151 GGAGAGGACC ATCTCTTTCA AGGACGACGG GAACTACAAG ACACGTGCTG
 1201 AAGTCAAGTT TGAGGGAGAC ACCCTCGTCA ACAGGATCGA GCTTAAGGGA
 1251 ATCGATTTCA AGGAGGACGG AATCATCTC GGCCACAAGT TGGAAATACAA
 1301 CTACAACCTC CACAACGTAT ACATCACGGC AGACAAACAA AAGAATGGAA
 1351 TCAAGCTAA CTTCAAAATT AGACACAACA TTGAAGATGG AAGCGTTCAA
 1401 CTAGCAGACC ATTATCAACA AAATACTCCA ATTGGCGATG GCCCTGTCTT
 1451 TTTACCAGAC AACCATTACC TGTCCACACA ATCTGCCCTT TCGAAAGATC
 1501 CCAACGAAAA GAGAGACCAC ATGGTCCTTC TTGAGTTTGT AACAGCTGCT
 1551 GGGATTACAC ATGGCATGGA TGAATATAC AAATAAGcct ctaga
 XbaI

aadA

dpp

Figure 31

FLARE11-S3.seq Length: 1961

1 SacI
 51 gaagctcGCTC CCCGCCGCTC GTTCAATGAG AATGGATAAG AGGCTCGTGG
 101 GATTGACGTG AGGGGGCAGG GATGGCTATA TTTCTGGGAG GGAGACCACA
 151 ATATGGCaAG CATGACTGGT GGACAGgcta gcgaacaaaa actcatttct
 201 gaagaagact tgcctagcGA AGCGGTGATC GCGGAAGTAT CGACTCAACT
 251 ATCAGAGGTA GTTGGCGTCA TCGAGCGCCA TCTCGAACCG ACGTTGCTGG
 301 CCGTACATTI GTACGGCTCC GCAGTGGATG GCGGCCTGAA GCCACACAGT
 351 GATATTGATT TGCTGGTTAC GGTGACCGTA AGGCTTGATG AAACAACCGC
 401 GCGAGCTTTG ATCAACGACC TTTTGAAAC TTCG3CTTCC CCTGGAGAGA
 451 GCGAGATTCT CCGCGCTGTA GAAGTACCA TTGTTGTGCA CGACGACATC
 501 ATTCCGTGGC GTTATCCAGC TAAGCGCGAA CTGCAATTG AGGATCTIAT
 551 GCGCAATGAC ATTCTTGCA GTATCTTCGA GCCAGCCACG ATCGACATTG
 601 ATCTGGCTAT CTTGCTGACA AAAGCAAGAG AACATAGCGT TGCCTTGGTA
 651 GGTCCAGCGG CCGAGGAACT CTTTGATCCG GTTCTGAAC AGGATCTIAT
 701 TGAGGCGCTA AATGAAACCT TAACGCTATG GAACTCGCCG CCCGACTGGG
 751 CTGGCGATGA GCGAATGTA GTGCTTACGT TGTCCCGCAT TTGGTACAGC
 801 GCAGTAACCG GCAAAATCGC GCCGAAGGAT GTCGCTGCCG ACTGGCGAT
 851 GGAGCGCCTG CCGGCCCACT ATCAGCGCGT CATACTTGAA GCTAGACAGG
 901 CTTATCTTGG ACAAGAAGAA GATCGCTTGG CCTCGCGCGC AGATCAGTTG
 951 GAAGAAATTTG TCCACTACGT GAAAGGCGAG ATCACCAGG TAGTgGGCAB
 1001 gaacttgca gttgaaggaa aattggaggt cggcATgct AGTAAAGGAG
 1051 AAGAACTTTT CACTGGAGTT GTCCCAATTC TTGTTGAATT AGATGGTGAT
 1101 GTTAATGGGC ACAAAATTTT TGTCAGTGA GAGGGTGAAG GTGATGCAAC
 1151 ATACGGAAAA CTTACCCTTA AATTATTG CACTACTGGA AACTACCTG
 1201 TTCCTTGGCC AACACTTGTC ACTACTTTCT CTTATGGTGT TCAATGCTTT
 1251 TCAAGATACC CAGATCATAT GAAGCGGCAC GACTTCTTCA AGAGCGCCAT
 1301 GCCTGAGGGA TACGTGCAGG AGAGGACCAT CTCTTTCAAG GACGACGGGA
 1351 ACTACAAGAC ACGTGTGAA GTCAAGTTTG AGGGAGACAC CCTCGTCAAC
 1401 AGGATCGAGC TTAAGGGAAT CGATTTCAG GAGGACGGAA ACATCCTCGG
 1451 CCACAAGTTG GAATACAAC AACTCCCA CAACGTATAC ATCAGCGCAG
 1501 ACAAAACAAA GAATGGAATC AAAGCTAACT TCAAAATTAG ACACAACATT
 1551 GAAGATGGAA GCGTTCACT AGCAGACCAT TATCAACAAA ATACTCCAAT
 1601 TGGCGATGGC CCTGTCCTTT TACCAGACAA CCATTACCTG TCCACACAAT
 1651 CTGCCCTTTT GAAAGATCCC AACGAAAAGA GAGACCACAT GGTCTTCTTT
 1701 GAGTTTGTA CAGCTGCTGG GATTACAT GGCATGGATG AACTATACAA
 1751 ATAAGctct agagcATCC TGGCCTAGTC TATAGGAGGT TTTGAAAAGA
 1801 AAGGAGCAAT AATCAATTTT TTGTTCTATC AAGAGGGTGC TATTGCTCCT
 1851 TTTCTTTTTT CTTTTTATTT ATTTACTAGT ATTTTACTTA CATAGACTTT
 1901 TTTGTTTACA TTATAGAAAA AGAAGGAGAG GTTATTTTCT TGCATTTATT
 1951 CATGaaagct t

HindIII

Figure 32

pMSK35.seq Length: 4671

Figure 33A

122488

1	GGGAACGGAT	TCACCGCGGT	ATGGCTGACC	GGCGATTACT	AGCGATTCTT
51	GCTTCATGCA	GGCGAGTTGC	AGCCTGCAAT	CCGAACCTGAG	GACGGGTTTT
101	TGGAGTTAGC	TCACCCCTCGC	GAGATCGCGA	CCCTTTGTCC	CGCCCAATTGT
151	AGCACGTGTG	TCGCCCAGGG	CATAAGGGGC	ATGATGACTT	GGCCTCATCC
201	TCTCCTTCCT	CCGGCTTAAC	ACCGGCGGTC	TGTTACGGGT	TCCAAACTCA
251	TAGTGGCAAC	TAAACACGAG	GGTTGCGCTC	GTTGCGAGAC	TTAACCCAAC
301	ACCTTACGGC	ACCGACTGAC	GACAGCCATG	CACCACCTGT	GTCCGCGTTC
351	CCGAGGGCAC	CCCTCTCTTT	CAAGAGGATT	CGCGGCATGT	CAAGCCCTGG
401	TAAGGTTCTT	CGCTTTGCA	CGAATTAAAC	CACATGCTCC	ACCGCTTGTG
451	CGGGCCCCCG	TCAATTCTT	TGAGTTTCAT	TCTTGCGAAC	GTAATCCCCA
501	GGCGGGATAC	TTAACGCGTT	AGCTACAGCA	CTGCACGGGT	CGAGTCGCAC
551	AGCACCTAGT	ATCCATCGTT	TACGGCTAGG	ACTACTGGGG	TCTCTAATCC
601	CATTTGCTCC	CCTAGCTTTC	GTCTCTCAGT	GTGAGTGTCC	GCCCAGCAGA
651	GTGCTTTGCG	CGTTGGTGT	CTTTCCGATC	TCAATGCATT	TACCCGCTCC
701	ACCGGAATTT	CCCTCTGCC	CTACCGTACT	CCAGTTGGT	AGTTTCCACC
751	GCCTGTCCAG	GGTTGAGCCC	TGGGATTGGA	CGGCGGACTT	GAAAAGCCAC
801	CTACAGACGC	TTTACGCCCC	ATCATTCGCG	ATAACGCTTG	CATCTCTGT
851	CTTACCGCGG	CTGCTGGCAC	AGAGTTAGCC	GATGCTTATT	CCTCAGATAC
901	CGTCATTGTT	TCTTCTCGA	GAAAAGAAGT	TGACGACCCG	TGGGCTTCC
951	ACCTCCACGC	GGCATTGCTC	CGTCAGGCTT	TCGCCCATTG	CGGAAATTC
1001	CCCCTGCTG	CCCTCCCGTAG	GAGTCTGGGC	CGTGTCTCAG	TCCCAGTGTG
1051	CTGTACTCAT	CTCTCGGACC	AGCTACTGAT	CATCGCCTTG	GTAAGCTATT
1101	GCCTCACCAA	CTAGCTAATC	AGACGCGAGC	CCCTCCTTGG	GCGGATTCT
1151	CCTTTTGTCT	CTCAGCCTAC	GGGGTATTAG	CAACCGTTTC	CAGTTGTTGT
1201	TCCCTCCCA	AGGGCAAGTT	CTTACGCGTT	ACTCACCCGT	TCGCCACTGG
1251	AAACACCACT	TCCCGTTTGA	CTTGCAATGT	TTAAGCATGC	CGCCAGCGTT
1301	CATCCTGAGC	CAGGATCGAA	CTCTCCATGA	GATTCATAGT	TGCATTACTT
1351	ATAGCTTCCT	TATTCGTAGA	CAAAGCGGAT	TCCGAATTGT	CTTTCCTTCC
1401	AAGGATAACT	TGTATCCATG	CGCTTCAGAT	TATTAGCCTG	GAGTTCGCCA
1451	CCAGCAGTAT	AGCCCAACCT	ACCTATCAC	GTCAATCCCA	CAAGCCTCTT
1501	ATCCATTCCG	GTTGATCGT	GGCGGGGGGA	GTAAGTCAAA	ATAGAAAAAA
1551	CTCACATTGG	GTTTAGGGAT	AATCAGGCTC	GAACTGATGA	CTTCCACCA
1601	GTCAAGGTGA	CACCTACCG	CTGAGTTATA	TCCCTTCCGC	GTCCCTCGA
1651	GAAAGAGAA	TAGCGAATCC	TAAGGCAAG	GGGCGAGAAA	CTCAAGGCCA
1701	CCCTTCTCC	GGGCTTTCTT	TCCACACTAT	TATGGATAGT	CAAATAATGG
1751	GAAAAATTGG	ATTCAATTGT	CAACCGGTCC	TATCGAAAA	AGGATTGACT
1801	ATGGATTGCA	GCCATAGCAC	ATGGTTTCAT	AAAATCTGTA	CGATTTTCCC
1851	GATCTAAATC	GAGCAGGTTT	CCATGAAGAA	gatcgacggt	atcgataagc
1901	ttgcatgcct	gcaggtCGAA	TATAGCTCTT	CTTTCTTATT	TCAATGATAT
1951	TATTATTTC	AAGATAAGAG	ATATTCAAAG	ATAAGAGATA	AGAAGAAGTC
2001	AAAATTTGAT	TTTTTTTTTG	GAAAAAAGAA	ATCAAAAAGA	TATAGTAACA
2051	TTAGCAAGAA	GAGAAACAAG	TCTATTTC	CAATTAAAC	AAATACAAA
2101	TCAAAATAGA	ATACTCAATC	ATGAATAAAT	GCAAGAAAA	AACTCTCCT
2151	TCTTTTTCTA	TAATGTAAAC	AAAAAAGTCT	ATGTAAGTAA	AACTACTAGT
2201	AATAAATAAA	AAGAAAAAAA	GAAAGGAGCA	ATAGCACCTC	CTTGATAGAA
2251	CAAGAAATAG	ATTATTGCTC	CTTTCTTTTC	AAAACCTCCT	ATAGACTAGG
2301	CCAGGATGgc	tetagcTAGA	CATTATTTC	CGACTACCTT	GGTGTCTCG
2351	CGTTTCAGT	AGTGGACAAA	TTCTTCCAAC	TGATCTGCGC	GCGAGGCCAA
2401	GCTACTTCT	TCTTGTCCAA	GATAAGCCTG	TCTAGCTTCA	AGTATGACGG
2451	GCTGATACTG	GGCCGGCAGG	CGCTCCATTG	CCAGTCGGC	AGCGACATCC
2501	TTGCGCGCGA	TTTTGCCGTT	TACTGCGCTG	TACCAAATGC	GGGACAACT
2551	AAGCACTACA	TTTCGCTCAT	CGCCAGCCCA	GTCGGGCGGC	GAGTTCCTCA
2601	CGGTTAAGGT	GCCTTTTAGC	GCCTCAAATA	GATCCTGTTT	AGGAACCGGA
2651	TCAAAGAGTT	CCTCCGCCGC	TGGACCTACC	AAGGCAACGC	TATGTTCTCT
2701	TGCTTTTGTG	AGCAAGATAG	CCAGATCAAT	GTCGATCGTG	GCTGGCTCGA

Rice left targeting sequence

aada

pMSK35.seq Length: 4671

pMSK35.seq Length: 4671

2751 AGATACCTGC AAGAATGTCA TTGCGCTGCC ATTCTCCAAA TTGCAGTTCG
 2801 CGCTTAGCTG GATAACGCCA CGGAATGATG TCGTCGTGCA CAACAATGGT
 2851 GACTTCTACA GCGCGGAGAA TCTCGCTCTC TCCAGGGGAA GCCGAAGTTT
 2901 CCAAAAAGTTC GTTGATCAAA GCTCGCCGCG TTGTTTCATC AAGCCTTACG
 2951 GTCACCGTAA CCAGCAAATC AATATCACTG TGTGGCTTCA GGCCGCCATC
 3001 CACTGCGGAG CCGTACAAAT GTACGCCAG CAACGTCGGT TCGAGATGGC
 3051 GCTCGATGAC GCCAACTACC TCTGATAGTT GAGTCGATAC TTCGGCGATC
 3101 ACCGCTTCCC TCATGgATCC CTCCCTACAA CTGTATCCAA GCGCTTCgTA
 3151 TTCGCCCGGA GTTCGCTCCC AGAAATATAG CCATCCCTGC CCCCTCACGT
 3201 CAATCCCACG AGCCTCTTAT CCATTCTCAT TGAACGACGG CGGGGGAGC
 3251 ttgggtaccg agctcgaatt cctgcagccc gatcTTACCA TTTCCGAAGG
 3301 AACTGGGGCT ACATTTCCTT TCAATTTCCA TTCAAGAGTT TCTTATCTGT
 3351 TTCCACGCCC TTTTTTGAGA CCTCGAAACA TGAATGGAC AAATTCCTTC
 3401 TCTTAGGAAC ACATACAAGA AAAAGGATAA TGGTAGCCCT CCCATTAAC
 3451 ACTTCATTTC ATTTATGAAT TTCATAGTAA TAGAAATCCA TGTCCTACCG
 3501 AGACAGAATT TCGAAGCTGC TATCCTCTTG CCTAATAGGC AAAGATTGAC
 3551 CTCTGTAGAA AGAATGATTC ATTGGATCG ATATGAGGAC CCAACTACGT
 3601 TGCATTGCGA AATCCATGTT CCATATTTGA AGAGGGTTGA CCTCTGTGCT
 3651 TCTCTCATGG TACAATCCTC TTCTGTCTGA GCCCCCTTTC TCCTCGGTCC
 3701 ACAGAGAAAA AATGGAGGAC TGGTGCAGAC AGTTCATCAC GGAAGAAAGA
 3751 ACTCACAGAG CCGGGATCGC TAACTAATAG AATAGTACTA CTAATAATA
 3801 CTATATATA GAAATAGATA Tctagctaga AATAGAAACA ACTAATATAT
 3851 AGATAACTGA AATTGAAAAG AACTGTCTTT TCTGTATACT TTCCCGTTTC
 3901 TATTGTACCC GCGGGTCTTA TGCAATCGAT CGGATCATAT AGATATCCCT
 3951 TCAACACAAC ATAGGTCATC GAAAGGATCT CGGACGACTC ACCAAAGCAC
 4001 GAAAGCCAGT TAGAAAATGG ATTCTATTTC GAAGAGTGCC TAACCGCATG
 4051 GATAAGCTCA CATTAACCCG TCAATTTTGG ATCCAATTCG GGATTTTCTC
 4101 TGGGAAGTTT CGGGAAGRAA TTGGAATGGA ATAATATAGA TTCATACAGA
 4151 GGAAAAGGTT CTCTATTGAT GCAAACGCTG TACCTAGAGG ATAGGGATAG
 4201 AGGAAGAGGG AAAAATCGAA ATGAAATAAA TAAAGAATAA AGCAAAAAAA
 4251 AAATAAGTCG AAGATAGAAG AGCCAGATT CCAATGAAG AAATGGAAC
 4301 TCGAAAAGGA TCCTTCTGAT TCTCAAAGAA TGAGGGGCAA GGGGATTGAT
 4351 ACCGAGAAAG ATTTCTTCTT ATTATAAGAC GTGATTTGAT CCGCATATGT
 4401 TTGGTAAAAA AACATCTTC TCCTTTAATC ATAAATGGAA AGTGTCAAT
 4451 TAGAACATGA AAACGTGACT CAATTGGTCT TAGTTAGTCT TCGGGACGGA
 4501 GTGGAAGAAA GGGCGAAGAC TCTCGAACGA GGAAAAGGAT CCCTTCGAAA
 4551 GAATTGAACG AGGAGCCGTA TTAGGTGAAA ATCTCATGTA CGATTCTGTA
 4601 GAGGGACAGG AAGGGTGACT TATCTGTGCA CTTTCCACT ATCAACCCCA
 4651 AAAAACCCTA CTCTGCCTTA C

aada
Rice Right-targeting sequence

125878

Figure 33B

pMSK49.seq Length: 5263

Figure 34A

122488

1	GGGAACGGAT	TCACCGCCGT	ATGGCTGACC	GGCGATTACT	AGCGATTCCCT
51	GCTTCATGCA	GGCGAGTTGC	AGCCTGCAAT	CCGAACTGAG	GACGGGTTTT
101	TGGAGTTAGC	TCACCGTCCG	GAGATCGCGA	CCCTTTGTCC	CGCCCATTTG
151	AGCACGTGTG	TCGCCCAGGG	CATAAGGGGC	ATGATGACTT	GGCCTCATCC
201	TCTCCTTCCT	CCGGCTTAAC	ACCGGCGGTC	TGTTCAGGGT	TCCAAACTCA
251	TAGTGGCAAC	TAAACACGAG	GGTTGCGCTC	GTTGCGAGAC	TTAACCCAAAC
301	ACCTTACGGC	ACGAGCTGAC	GACAGCCATG	CACCACCTGT	GTCCGCGTTC
351	CCGAGGGCAC	CCCTCTCTTT	CAAGAGGATT	CGCGCATGCT	CAAGCCCTGG
401	TAAGTTCTT	CGCTTTGCAT	CGAATTAAC	CACATGCTCC	ACCCTTTGTG
451	CGGGCCCCCG	TCAATTCCTT	TEAGTTTCAT	TCTTGCGAAC	GTACTCCCCA
501	GGCGGGATAC	TTAACGCGTT	AGCTACAGCA	CTGCACGGGT	CGAGTCGCAC
551	AGCACCTAGT	ATCCATCGTT	TACGGCTAGG	ACTACTGGGG	TCTCTAATCC
601	CATTTGCTCC	CCTAGCTTTC	GTCTCTCAGT	GTGAGTGTG	CGCCAGCAGA
651	GTGCTTTGCG	CGTTGGTGT	CTTTCCGATC	TCAATGCATT	TCACCGCTCC
701	ACCGGAAATT	CCCTCTGCCC	CTACCGTACT	CCAGCTTGCT	AGTTTCCACC
751	GCCTGTCCAG	GGTTGAGCCC	TGGGATTTGA	CGGCGGACTT	GAAAGCCAC
801	CTACAGACGC	TTTACGCCCA	ATCATTCCGG	ATAACGGCTT	CATCTCTGT
851	CTTACCGCGG	CTGCTGGCAC	AGAGTTAGCC	GATGCTTATT	CCTCAGATAC
901	CGTCAATTGT	TCTTCTCCGA	GAAAGAAGT	TGACGACCCG	TGGGCCCTTC
951	ACCTCCACGC	GGCATTTGCT	CGTCAGGCTT	TCGCCCATTG	CGGAAAATTG
1001	CCCTACTGCTG	CCTCCCGTAG	GAGTCTGGGC	CGTGTCTCAG	TCCCAGTGTG
1051	GCTGATCATC	CTCTCGGACC	AGCTACTGAT	CATCGCCTTG	GTAAAGCTATT
1101	GCCTCACCAA	CTAGCTAATC	AGACGCGAGC	CCCTCCTTGG	GCGGATTTCT
1151	CCCTTTTGCTG	CTCAGCCTAC	GGGGTATTAG	CAACCGTTTT	CAGTTGTTGT
1201	TCCCTCCCA	AGGGCAGJTT	CTTACGCGTT	ACTCACCCGT	TCGCCACTGG
1251	AAACACCATT	TCCCGTTTGA	CTTGCATGTG	TTAAGCATGC	CGCCAGCGTT
1301	CATCCTGAGC	CAGGATCGAA	CTCTCCATGA	GATTCATAGT	TGCATTACTT
1351	ATAGCTTCCT	TATTCCTAGA	CAAAGCGGAT	TCGGAATTGT	CTTTCCTTCC
1401	AAGGATAACT	TGTATCCATG	CGCTTCAGAT	TATTAGCCTG	GAGTTCGCCA
1451	CCAGCAGTAT	AGCCAACCCCT	ACCCTATCAC	GTCAATCCCA	AGACCTCTTT
1501	ATCCATTCCC	GTTTCGATCGT	GGCGGGGGGA	GTAAGTCAAA	ATAGAAAAAA
1551	CTCACATTGG	GTTTAGGGAT	AATCAGGGCTC	GAACGTGATG	CTTCCACCAC
1601	GTCAGGTGA	CACCTTACCG	CTGAGTTATA	TCCCTTCCCC	GTCCCTTCGA
1651	GAAAGAGAAAT	TACCGAATCC	TAAGGCAAAAG	GGGCGAGAAA	CTCAAGGCCA
1701	CCCTTCTCTC	GGGCTTTCTT	TCCACACTAT	TATGGATAGT	CAAATAATGG
1751	GAAAAATTGG	ATTCAATTGT	CAACCGGTCC	TATCGAAAAAT	AGGATTGACT
1801	ATGGATTGCA	GCCATAGCAC	ATGGTTTCAT	AAAATCTGTA	CGATTTTCCC
1851	GATCTAAATC	GAGCAGGTTT	CCATGAAGAA	gatcgacggt	atcgataagc
1901	TTTCTATGAT	AAATGCAAGA	AAATAACCTC	TCCTTCTTTT	TCTATAATGT
1951	AAACAAAAAA	GTCTATGTAA	GTAATAACT	AGTAAATAAA	TAAAAAGAAA
2001	AAAGAAAGG	AGCAATAGCA	COCTTTGAT	AGAACAAGAA	AATGATTATT
2051	GCTCCTTTCT	TTTCBAABACC	TCCTATAGAC	TAGGCCAGGA	TCgctctaga
2101	gcTTATTATT	TATAGTTTCAT	CCATGCCATG	TGTAATCCCA	GCAGCTGTTA
2151	CAAACTCAAG	AAGGACCATG	TGGTCTCTCT	TTTCGTTGGG	ATCTTTCGAA
2201	AGGGCAGATT	GTGTGGACAG	GTAATGGTTG	TCTGGTAAAA	GGACAGGGCC
2251	ATCGCCAATT	GGAGTATTTT	GTTGATAATG	GTCTGCTAGT	TGAACGCTTC
2301	CATCTTCAAT	GTTGTGTCTA	ATTTTGAAGT	TAGCTTTGAT	TCCATTCTTT
2351	TGTTTGTCTG	COGTGTGATG	TACGTTGTGG	GAGTTGTAGT	TGTATTCCAA
2401	CTTGTGGCCG	AGGATGTTTC	CGTCCCTCCT	GAAATCGATT	CCCTTAAGCT
2451	CGATCCTGTT	GACGAGGGTG	TCTCCCTCAA	ACTTGACTTC	AGCACGTGTC
2501	TGTGTAGTCC	CGTCTCCTT	GAAAGAGATG	GTCCTCTCCT	GCACGTATCC
2551	CTCAGGCATG	GCGCTCTTGA	AGAAGTCGTG	CCGCTTCATA	TGATCTGGGT
2601	ATCTTGAAAA	GCATTGAACA	CCATAAGAGA	AAGTAGTGAC	AAGTGTGGCC
2651	CAAGGAACAG	GTAGTTTTC	AGTAGTGCAA	ATAAATTTAA	GGGTAAGTTT
2701	TCCGTATGTT	GCATCACCTT	CACCCCTCTC	ACTGCACAGAA	AATTTGTGCC

Rice left targeting Sequence

185A

245A

09762105.042904

Figure 34B

pMSK49.seq Length: 5263

2751	CATTAACATC	ACCATCTAAT	TCAACAAGAA	TTGGGACBAC	TCCAGTGAAB
2801	AGTTCTCTCTC	CTTTACTAGC	CATggcgacc	tccaattttc	cttcaactgc
2851	aaattcttTG	CCACTACCT	TGGTGATCTC	GCCTTTCACG	TAGTGGACAA
2901	ATTCTTCCAA	CTGATCTGCG	CGCGAGGCCA	AGCGATCTTC	TTCTTGCCA
2951	AGATAAGCCT	GTCTAGCTTC	AAGTATGACG	GGCTGATACT	GGGCCGGCAG
3001	GCGCTCCATT	GCCCAGTCGG	CAGCGACATC	CTTCGGCGCG	ATTTTGCCCG
3051	TTACTGCGCT	GTACCAAAATG	CGGGACAACG	TAAGCACTAC	ATTTTCGCTCA
3101	TCGCCAGCCC	AGTCGGGCGG	CGAGTTCCAT	AGCGTTAAGG	TTTCATTTAG
3151	CGCCTCAAAT	AGATCCTGTT	CAGGAACCGG	ATCAAAGAGT	TCCTCCGCGG
3201	CiGGACCTAC	CAAGGCAACG	CTATGTTCTC	TTGCTTTTGT	CAGCAAGATA
3251	GCCAGATCAA	TGTCGATCGT	GGCTGGCTCG	AAGATACCTG	CAAGAAATGTC
3301	ATTGCGCTGC	CATTCTCCAA	ATTGCACTTC	GCGCTTAGCT	GGATAACGCC
3351	ACGGAATGAT	GTCGTGCTGC	ACAACAATGG	TGACTTCTAC	AGCGCGGAGA
3401	ATCTCGCTCT	CTCCAGGGGA	AGCCGAAGTT	TCCAAAAGGT	CGTTGATCAA
3451	AGCTCGCGCG	GTTGTTTCAT	CAAGCCTTAC	GGTCACCGTA	ACCAGCAAAT
3501	CAATATCACT	GTGTGGCTTC	AGGCCGCCAT	CCACTCGGGA	GCCGTACAAAT
3551	TGTACGGCCA	GCAACGTCGG	TTGAGATGG	CGCTCGATGA	CGCCAACTAG
3601	CTCTGATAGT	TGAGTCGATA	CTTCGGCGAT	CACCGCTTCg	ctaggccaagt
3651	cttcttcaga	aatgagtttt	tgttcgctag	CTGTCCACC	AGTCATGCTT
3701	GCCATATGTA	TATCTCCTTC	TTAAGTTAA	ACAAAATTAT	TTCTAGTGGG
3751	AAACCGTTGT	GGTCTCCCTC	CCAGAAATAT	AGCCATCCCT	GCCCCCTCAC
3801	GTAACCCCA	CGAGCCTCTT	ATCCATTCTC	ATTGAACGAC	GGCGGGGGAG
3851	cyagctcgaa	ttcctgcagc	ccgataTTAC	CATTTTCGAA	GCAACTGGGG
3901	CTACATTTCT	TTTCAATTTT	CATTCAAGAG	TTTCTTATCT	GTTTCCACCG
3951	CCTTTTTTGA	GACCTCGAAA	CATGAAATGG	ACAAATTCCT	TCTCTTAGGA
4001	ACACATACAA	GAATAAGGAT	AATGGTAGCC	CTCCCATTAA	CTACTTCATT
4051	TCATTTATGA	ATTTCATAGT	AATAGAAATC	CATGTCCTAC	CGAGACAGAA
4101	TTTCGAACCT	GCTATCCTCT	TGCTTAATAG	GCAAGAGATTG	ACCTCTGTAG
4151	AAAGAATGAT	TCATTCCGGAT	CGATATGAGG	ACCCAACCTAC	GTTGCATTGC
4201	AGAATCCATG	TTCCATATTT	GAAGAGGGTT	GACTCTGTG	CTTCTCTCAT
4251	GGTACAATCC	TCTTCCTGCT	GAGCCCCCTT	TCTCCTCGGT	CCACAGAGAA
4301	AAAATGGAGG	ACTGGTGCCG	ACAGTTTCATC	ACGGAAGAAA	GAATCTACAG
4351	AGCCGGGATC	GCTAATAAT	AGAATAGTAC	TACTAATAA	TACTAATATA
4401	TAGAAATAGA	TATctagcta	gAAATAGAAA	CACTAATAT	ATAGATAATC
4451	GAATTTGAAA	AGAATGTCT	TTTCTGTATA	CTTCCCTCT	TCTATTGCTA
4501	CCGCGGGTCT	TATGCAATCG	ATCGGATCAT	ATAGATATCC	CTTCAACACA
4551	ACATAGGTCA	TCGAAAGGAT	CTCGGACGAC	TCACCAAAAGC	ACGAAAAGCCA
4601	GTTAGAAAAAT	GGATTCCCTAT	TTGAAGAGTG	CCTAACCCGA	TGGATAAGCT
4651	CACATTAAAC	CGTCAATTTT	GGATCCAATT	CGGATTTTT	CTTGGGAAGT
4701	TTCCGGGAAG	AATTGGAATG	GAATAATATA	GATTCAATCA	GAGGAAAAGG
4751	TTCTCTATTG	ATGCAAAACG	TGTACCTAGA	GGATAGGGAT	AGAGGAAGAG
4801	GGAAAAATCG	AAATGAAATA	AATAAAGAAAT	AAAGCAAAAA	AAAAATAAGT
4851	CGAAGATAGA	AGAGCCGAGA	TTCCAAATGA	AGAAATGGAA	ACTCGAAAAG
4901	GATCCTTCTG	ATTCTCAAAG	AATGAGGGGC	AAGGGGATTG	ATACCGAGAA
4951	AGATTCTTCT	TTATTATAAG	ACGTGATTTG	ATCCGCATAT	GTTTGGTAAA
5001	AGAACATCT	TCTCCTTTAA	TCATAAATGG	AAAGTGTTC	ATTAGAACAT
5051	GAAACGTGA	CTCAATTGGT	CTTAGTTAGT	CTTCGGGACG	GAGTGAAGAA
5101	AAGGGCGAAG	ACTCTCGAAC	GAGGAAAAGG	ATCCCTTCGA	AAGAATTGAA
5151	CGAGGAGCCG	TATTAGGTGA	AAATCTCATG	TACGATTCTG	TAGAGGGACA
5201	GGAAGGGTGA	CTTATCTGTC	GACTTTTCCA	CTATCAACCC	CAAAAAACCC
5251	AACTCTGCCT	TAG			

oada

L7910DB

Rice Right targeting sequence.

125878

09762105 012301

Gene	Product	Plasmid
<i>aadA16gfp</i>	FLARE16-S	pMSK51 (BS)
<i>aadA16gfp-S1</i>	FLARE16-S1	pMSK56 (Nt-pRV111B)
<i>aadA16gfp-S2</i>	FLARE16-S2	pMSK57 (Nt-pRV111B)
<i>aadA11gfp-S3</i>	FLARE11-S3	pMSK49 (Os-pMSK49)

Figure 35